



2618-17-C4-PUS-2.txt  
SEQUENCE LISTING

The following Sequence Listing is submitted pursuant to CFR 1.821. A copy in computer readable form is also submitted herewith.

Applicants assert pursuant to 37 CFR 1.821(f) that the content of the paper and computer readable copies of SEQ ID NO:1 through SEQ ID NO:88 submitted herewith are the same.

(1) GENERAL INFORMATION:

- (i) APPLICANT: Frank, Glenn R.  
Wu Hunter, Shirley  
Wallenfels, Lynda
- (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
- (iii) NUMBER OF SEQUENCES: 88
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SHERIDAN ROSS P.C.
  - (B) STREET: 1700 LINCOLN ST., SUITE 3500
  - (C) CITY: DENVER
  - (D) STATE: CO
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Connell, Gary J.
  - (B) REGISTRATION NUMBER: 32,020
  - (C) REFERENCE/DOCKET NUMBER: 2618-17-C4
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 303/863-9700
  - (B) TELEFAX: 303/863-0223

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr  
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Tyr or Asp
- (B) LOCATION: 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg  
1 5 10 15

Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln  
20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 8

(ix) FEATURE:

- (A) NAME/KEY: Xaa = Ala or His
- (B) LOCATION: 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu  
1 5 10 15

Arg Val Leu Asp Pro Ser Lys  
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys  
1 5 10 15

Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp  
 1 5 10 15

Glu Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Phe Asn Asp Gln Ile Lys Ser Val Met Glu Pro Xaa Val Phe Lys  
 1 5 10 15

Tyr Pro Xaa Ala Xaa Leu  
 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGRTTTCCWA TRAARTCTTC

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTACATT AAATTTTCA AATTCGATAT

60

GAAATTTTA CTGGCAATTG	120
GCCTGTTGTG TGTTTATTAA ATCAAGTAT CTATGTCAA	
AATGGTCACT GAAAAGTGTAA AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT	180
ACCATCTGGG AAGCTTACTA TTGAAGATTGTTGTATTGGA AATCA	225

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /label= primer

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCGGCAC GAGTG	15
------------------	----

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 565 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 45..314

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAATTCAA TATTTGTTT TACATTAAT TTTCAAATT CGAT ATG AAA TTT TTA	56
Met Lys Phe Leu	
1	

CTG GCA ATT TGC GTG TTG TGT GTT TTA AAT CAA GTA TCT ATG TCA	104
Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met Ser	
5 10 15 20	

AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA	152
Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr	
25 30 35	

GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys 40 45 50	200
ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly 55 60 65	248
TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn Gln 70 75 80	296
AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG Lys His Cys Tyr Cys Glu 85 90	344
ATATAAAATTA CTAAAATTAT GCTAGATAGC AATCATAAAA TTTTGAAGTT TTCAATGATC	404
CTAACATGTT TTGCCTCCAA TTTATTTAA CAGCAAATTG CTGGAACTTA CCGTACCGTA	464
ACTAAATGTT CAAGAAATAC TGAATGTTA CAAATAGATT ATTATAAATA TTGTAACATT	524
GTCTAATATT TATAAGAATT ATATAAACTG AATTGCAAAA A	565

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln 1 5 10 15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn 20 25 30
Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 35 40 45
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 50 55 60
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr 65 70 75 80
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 85 90

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln 1 5 10 15	48
GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn 20 25 30	96
AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile 35 40 45	144
GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys 50 55 60	192
AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr 65 70 75 80	240
CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA Arg Pro Asn Gln Lys His Cys Tyr Cys Glu 85 90	270

(2) INFORMATION FOR SEQ ID NO:14:

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Phe	Leu	Leu	Ala	Ile	Cys	Val	Leu	Cys	Val	Leu	Leu	Asn	Gln
1									10					15	
Val	Ser	Met	Ser	Lys	Met	Val	Thr	Glu	Lys	Cys	Lys	Ser	Gly	Gly	Asn
									20			25		30	
Asn	Pro	Ser	Thr	Glu	Glu	Val	Ser	Ile	Pro	Ser	Gly	Lys	Leu	Thr	Ile
									35			40		45	

2618-17-C4-PUS-2.txt  
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys  
50 55 60  
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr  
65 70 75 80  
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..26
  - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTGGATCCG TCAAAATGG TCACTG

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..28
  - (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGGAATTCG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 897 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGAAATCTC CTATCACAGT GTACGGAGTG TAAAATATTG TTGAAGTATT TTGAAATTTA	60
TTAATTTATT CGAAAAGGAG ATTCATTAAT TAC GAA AGT GAC Met Val Tyr Glu Ser Asp	114
1 5	
TTT TAC ACG ACC CGT CGG CCC TAC AGT CGT CCG GCT TTG TCT TCA TAC Phe Tyr Thr Arg Arg Pro Tyr Ser Arg Pro Ala Leu Ser Ser Tyr	162
10 15 20	
TCC GTA ACG GCA CGT CCA GAG CCG GTT CCT TGG GAC AAA TTG CCG TTC Ser Val Thr Ala Arg Pro Glu Pro Val Pro Trp Asp Lys Leu Pro Phe	210
25 30 35	
GTC CCC CGT CCA AGT TTG GTA GCA GAT CCC ATA ACA GCA TTT TGC AAG Val Pro Arg Pro Ser Leu Val Ala Asp Pro Ile Thr Ala Phe Cys Lys	258
40 45 50	
CGA AAA CCT CGC CGA GAA GAA GTT GTT CAA AAA GAG TCC ATT GTT CGA Arg Lys Pro Arg Arg Glu Glu Val Val Gln Lys Glu Ser Ile Val Arg	306
55 60 65 70	
AGG ATC AAT TCT GCA GGA ATT AAA CCC AGC CAG AGA GTT TTA TCG GCT Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser Gln Arg Val Leu Ser Ala	354
75 80 85	
CCA ATA AGA GAA TAC GAA TCC CCA AGG GAC CAG ACC AGG CGT AAA GTT Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp Gln Thr Arg Arg Lys Val	402
90 95 100	
TTG GAA AGC GTC AGA AGA CAA GAA GCT TTT CTG AAC CAA GGA GGA ATT Leu Glu Ser Val Arg Arg Gln Glu Ala Phe Leu Asn Gln Gly Gly Ile	450
105 110 115	
TGT CCA TTG ACC ACC AGA AAT GAT GAC ATG GAT AGA CTT CTA CCC CGT Cys Pro Leu Thr Thr Arg Asn Asp Asp Met Asp Arg Leu Leu Pro Arg	498
120 125 130	
CTC CAC AGT TCA CAC ACA ACA CCT TCT GCG GAT AGG AAA GTT TTG TTG Leu His Ser Ser His Thr Thr Pro Ser Ala Asp Arg Lys Val Leu Leu	546
135 140 145 150	
ACC ACT TTT CAC AGA AGA TAC T GATTAAAAAT GAAAGTTAAG AAATTTGTTG Thr Thr Phe His Arg Arg Tyr	598
155	
AAGTCATGTG GTGTTTTTA TACATTCTTT ATTAATCGAT ATTCCTAACG AACGATAACGA	658
TAACTTCGA TAACTTTTC TGTTAATT TGACAAAATA TGCATTTGCA AGCATAACAT	718

TCATTTCAA GGCAAACGCT TTCTGATGAT TATCTTGTAA AAAGTGTGGA AACAAAGCGTA	778
GTGTTAACAA ATGCATTGCT TGTTTGATT ATTTATTTAT CTATTATATA TTCCATATTG	838
TATTGTAGGT GGTGTACTTG GTATTACTAA TACACGTACT TTGTGAAAAA AAAAAAAA	897

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Val Tyr Glu Ser Asp Phe Tyr Thr Thr Arg Arg Pro Tyr Ser Arg			
1	5	10	15
Pro Ala Leu Ser Ser Tyr Ser Val Thr Ala Arg Pro Glu Pro Val Pro			
20	25	30	
Trp Asp Lys Leu Pro Phe Val Pro Arg Pro Ser Leu Val Ala Asp Pro			
35	40	45	
Ile Thr Ala Phe Cys Lys Arg Lys Pro Arg Arg Glu Glu Val Val Gln			
50	55	60	
Lys Glu Ser Ile Val Arg Arg Ile Asn Ser Ala Gly Ile Lys Pro Ser			
65	70	75	80
Gln Arg Val Leu Ser Ala Pro Ile Arg Glu Tyr Glu Ser Pro Arg Asp			
85	90	95	
Gln Thr Arg Arg Lys Val Leu Glu Ser Val Arg Arg Gln Glu Ala Phe			
100	105	110	
Leu Asn Gln Gly Gly Ile Cys Pro Leu Thr Thr Arg Asn Asp Asp Met			
115	120	125	
Asp Arg Leu Leu Pro Arg Leu His Ser Ser His Thr Thr Pro Ser Ala			
130	135	140	
Asp Arg Lys Val Leu Leu Thr Thr Phe His Arg Arg Tyr			
145	150	155	

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGTTTACG AAAGTGACTT TTACACGACC CGTCGGCCCT ACAGTCGTCC GGCTTTGTCT	60
TCATACTCCG TAACGGCACG TCCAGAGCCG GTTCCTTGGG ACAAAATTGCC GTTCGTCCCC	120
CGTCCAAGTT TGGTAGCAGA TCCCATAACA GCATTTGCA AGCGAAAACC TCGCCGAGAA	180
GAAGTTGTTA AAAAAGAGTC CATTGTTCGA AGGATCAATT CTGCAGGAAT TAAACCCAGC	240
CAGAGAGTTT TATCGGCTCC AATAAGAGAA TACGAATCCC CAAGGGACCA GACCAGGCGT	300
AAAGTTTGG AAAGCGTCAG AAGACAAGAA GCTTTCTGA ACCAAGGAGG AATTGTCCA	360
TTGACCACCA GAAATGATGA CATGGATAGA CTTCTACCCC GTCTCACAG TTCACACACA	420
ACACCTTCTG CGGATAGGAA AGTTTGTTG ACCACTTTTC ACAGAAGATA C	471

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..2706

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGG ATG AAG AGC ATC GAG GCT TAT ACA AAC AGA TAT GAA ATC ATA GCT	49
Met Lys Ser Ile Glu Ala Tyr Thr Asn Arg Tyr Glu Ile Ile Ala	
1 5 10 15	

TCT GAA ATA GTT AAT CTT CGA ATG AAA CCA GAT GAT TTT AAT TTA ATA	97
Ser Glu Ile Val Asn Leu Arg Met Lys Pro Asp Asp Phe Asn Leu Ile	
20 25 30	

AAA GTT ATT GGT CGA GGA GCA TTT GGT GAA GTA CAG TTA GTG CGA CAC	145
Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His	
35 40 45	

AAA TCA ACT GCA CAA GTT TTT GCT ATG AAA CGC CTA TCA AAA TTT GAA	193
Lys Ser Thr Ala Gln Val Phe Ala Met Lys Arg Leu Ser Lys Phe Glu	
50 55 60	

ATG ATT AAG AGA CCA GAC TCT GCA TTT TTT TGG GAA GAA CGT CAT ATA	241
Met Ile Lys Arg Pro Asp Ser Ala Phe Phe Trp Glu Glu Arg His Ile	
65 70 75	

ATG GCT CAT GCA AAA TCA GAA TGG ATT GTA CAA TTA CAT TTT GCT TTT	289
---	-----

## 2618-17-C4-PUS-2.txt

Met Ala His Ala Lys Ser Glu Trp Ile Val Gln Leu His Phe Ala Phe			
80	85	90	95
CAA GAT CAA AAA TAT CTT TAT ATG GTC ATG GAT TAT ATG CCG GGG GGT			337
Gln Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly			
100	105	110	
GAC TTG GTG AGT CTT ATG TCC GAT TAT GAA ATT CCA GAA AAA TGG GCA			385
Asp Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala			
115	120	125	
ATG TTC TAT ACA ATG GAA GTG GTG CTA GCA CTT GAT ACA ATT CAC TCC			433
Met Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser			
130	135	140	
ATG GGA TTT GTA CAT CGT GAT GTT AAA CCT GAT AAT ATG CTT CTA GAC			481
Met Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp			
145	150	155	
AAA TAT GGT CAT TTA AAG TTA GCT GAC TTT GGA ACC TGT ATG AAA ATG			529
Lys Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met			
160	165	170	175
GAT ACA GAT GGT TTG GTA CGT TCT AAT AAT GCT GTT GGA ACG CCT GAT			577
Asp Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp			
180	185	190	
TAC ATT TCT CCC GAA GTT TTG CAG TCC CAA GGT GGT GAA GGA GTT TAC			625
Tyr Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Glu Gly Val Tyr			
195	200	205	
GGT CGT GAA TGC GAT TGG TGG TCT GTG GGA ATT TTT TTG TAT GAA ATG			673
Gly Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met			
210	215	220	
TTA TTT GGA GAA ACA CCT TTT TAT GCA GAC AGT TTG GTT GGA ACT TAC			721
Leu Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr			
225	230	235	
AGT AAA ATT ATG GAT CAC AGA AAC TCA TTA ACT TTT CCT CCA GAA GTG			769
Ser Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val			
240	245	250	255
GAA ATA AGC CAA TAT GCC CGA TCT TTG ATA CAA GGA TTT TTA ACA GAC			817
Glu Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp			
260	265	270	
AGA ACA CAG CGT TTA GGC AGA AAT GAA GTG GAA GAA ATT AAA CGA CAT			865
Arg Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Ile Lys Arg His			
275	280	285	
CCA TTT TTC ATA AAT GAT CAA TGG ACT TTT GAC AAT TTA AGA GAC TCT			913
Pro Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser			
290	295	300	
GCC CCA CCT GTA GTG CCA GAG CTG AGT GGT GAT GAT GAT ACA AGG AAC			961
Ala Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn			
305	310	315	

## 2618-17-C4-PUS-2.txt

TTT GAT GAT ATT GAA CGT GAT GAA ACA CCT GAA GAG AAT TTT CCT ATA Phe Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile 320 325 330 335	1009
CCA AAA ACT TTT GCT GGT AAT CAT CTG CCA TTT GTT GGA TTC ACA TAT Pro Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr 340 345 350	1057
AAT GGT GAT TAC CAA TTA TTA ACA AAT GGA GGT GTT AGA AAT AGT GAT Asn Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp 355 360 365	1105
ATG GTT GAT ACA AAA TTA AAC AAC ATT TGT GTT TCA AGT AAG GAT GAT Met Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp 370 375 380	1153
GTG TTA AAT TTA CAA AAT TTA TTA GAA CAA GAG AAA GGT AAC AGT GAA Val Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu 385 390 395	1201
AAT TTG AAA ACA AAC ACC CAA TTA TTA AGT AAT AAA TTA GAT GAA CTA Asn Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu 400 405 410 415	1249
GGT CAG AGA GAA TGT GAA TTA AGG AAT CAG GCT GGA GAT TAT GAG AAA Gly Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys 420 425 430	1297
GAA TTG ACT AAA TTC AAA TTA TCG TGC AAA GAA TTA CAA CGT AAG GCA Glu Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala 435 440 445	1345
GAA TTT GAG AAT GAA TTA CGG CGT AAA ACT GAG TCC TTA CTA GTT GAA Glu Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu 450 455 460	1393
ACA AAG AAA AGA CTA GAC GAA GAG CAG AAT AAA AGA ACT AGA GAA ATG Thr Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met 465 470 475	1441
AAT AAT AAT CAA CAG CAC AAT GAC AAA ATA AAT ATG TTA GAA AAA CAA Asn Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln 480 485 490 495	1489
ATT AAT GAT TTA CAA GAA AAA TTG AAA GGT GAA TTA GAG CAC AAT CAG Ile Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln 500 505 510	1537
AAA TTA AAG AAG CAA GCT GTT GAG CTT AGA GTT GCT CAG TCT GCT ACT Lys Leu Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr 515 520 525	1585
GAA CAA CTG AAT AAT GAA TTA CAG GAA ACT ATG CAG GGT TTA CAA ACA Glu Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr 530 535 540	1633
CAA AGA GAT GCT TTA CAA CAA GAA GTA GCA TCT CTC CAA GGC AAA CTT Gln Arg Asp Ala Leu Gln Gln Glu Val Ala Ser Leu Gln Gly Lys Leu 545 550 555	1681

TCT CAA GAG AGG AGC TCT AGA TCA CAG GCT TCT GAT ATG CAG ATA GAA Ser Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu 560 565 570 575	1729
CTA GAA GCA AAA TTG CAG GCT CTC CAT ATT GAA CTG GAG CAT GTC AGA Leu Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg 580 585 590	1777
AAT TGT GAA GAC AAA GTT ACC CAA GAC AAC AGA CAA CTA TTG GAA AGG Asn Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg 595 600 605	1825
ATA TCA ACA TTG GAG AAA GAA TGT GCT TCT CTA GAA TTA GAA TTG AAA Ile Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys 610 615 620	1873
GCA ACA CAA AAC AAA TAT GAG CAA GAG GTC AAA GCA CAT CGC GAA ACT Ala Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr 625 630 635	1921
GAA AAA TCA AGA CTG GTC AGT AAA GAA GAA GCA AAT ATG GAG GAA GTT Glu Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val 640 645 650 655	1969
AAA GCA CTC CAA ATA AAA TTA AAT GAA GAG AAA TCT GCT CGA CAG AAA Lys Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys 660 665 670	2017
TCT GAT CAG AAT TCT CAA GAA AAG GAA CGA CAA ATT TCT ATG TTA TCT Ser Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser 675 680 685	2065
GTG GAT TAT CGT CAA ATC CAA CAG CGT TTG CAA AAG CTA GAA GGA GAA Val Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu 690 695 700	2113
TAT AGG CAA GAG AGT GAA AAA GTT AAA GCT CTC CAC AGT CAG ATT GAG Tyr Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu 705 710 715	2161
CAA GAG CAA CTA AAA AAA TCA CAA TTA CAA AGC GAA TTG GGT GTT CAA Gln Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln 720 725 730 735	2209
AGG TCT CAG ACT GCA CAT TTA ACA GCC AGG GAA GCT CAG CTA GTT GGA Arg Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly 740 745 750	2257
GAA GTT GCT CAT CTT AGA GAT GCT AAA AGA AAT GTT GAA GAA GAG TTA Glu Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Leu 755 760 765	2305
CAC AAG TTA AAA ACT GCT CGA TCA GTG GAT AAT GCT CAG ATG AAA GAG His Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu 770 775 780	2353
CTT CAA GAA CAA GTT GAA GCC GAG CAA GTT TTC TCG ACT CTT TAT AAA Leu Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys	2401

785	790	795	
ACA CAT TCT AAT GAA CTT AAG GAA GAA CTT GAG GAA AAA TCT CGT CAT			
Thr His Ser Asn Glu Leu Lys Glu Leu Glu Lys Ser Arg His			
800	805	810	815
ATT CAA GAA ATG GAA GAA AGA GAA AGT TTG GTT CAT CAG CTA CAA			
Ile Gln Glu Met Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln			
820	825	830	
ATT GCA TTA GCT AGA GCT GAT TCA GAG GCA TTG GCG AGA TCA ATA GCT			
Ile Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala			
835	840	845	
GAT GAA AGT ATA GCT GAT TTA GAA AAG GAA AAG ACT ATG AAG GAA TTA			
Asp Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu			
850	855	860	
GAA CTA AAA GAA TTA TTA AAC AAA AAT CGT ACT GAA CTT TCC CAG AAA			
Glu Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys			
865	870	875	
GAC ATT TCA ATA AGT GCA TTG CGT GAA CGA GAA AAT GAA CAG AAG AAA			
Asp Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys			
880	885	890	895
CTT TTA GAA CAA ATC TC			
Leu Leu Glu Gln Ile			
900			

## (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Lys	Ser	Ile	Glu	Ala	Tyr	Thr	Asn	Arg	Tyr	Glu	Ile	Ile	Ala	Ser
1				5				10				15			
Glu	Ile	Val	Asn	Leu	Arg	Met	Lys	Pro	Asp	Asp	Phe	Asn	Leu	Ile	Lys
		20				25						30			
Val	Ile	Gly	Arg	Gly	Ala	Phe	Gly	Glu	Val	Gln	Leu	Val	Arg	His	Lys
		35			40				40			45			
Ser	Thr	Ala	Gln	Val	Phe	Ala	Met	Lys	Arg	Leu	Ser	Lys	Phe	Glu	Met
		50			55				55			60			
Ile	Lys	Arg	Pro	Asp	Ser	Ala	Phe	Phe	Trp	Glu	Glu	Arg	His	Ile	Met
		65			70				75			80			
Ala	His	Ala	Lys	Ser	Glu	Trp	Ile	Val	Gln	Leu	His	Phe	Ala	Phe	Gln
			85			90			90			95			

2618-17-C4-PUS-2.txt

Asp Gln Lys Tyr Leu Tyr Met Val Met Asp Tyr Met Pro Gly Gly Asp  
100 105 110

Leu Val Ser Leu Met Ser Asp Tyr Glu Ile Pro Glu Lys Trp Ala Met  
115 120 125

Phe Tyr Thr Met Glu Val Val Leu Ala Leu Asp Thr Ile His Ser Met  
130 135 140

Gly Phe Val His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys  
145 150 155 160

Tyr Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asp  
165 170 175

Thr Asp Gly Leu Val Arg Ser Asn Asn Ala Val Gly Thr Pro Asp Tyr  
180 185 190

Ile Ser Pro Glu Val Leu Gln Ser Gln Gly Gly Glu Gly Val Tyr Gly  
195 200 205

Arg Glu Cys Asp Trp Trp Ser Val Gly Ile Phe Leu Tyr Glu Met Leu  
210 215 220

Phe Gly Glu Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser  
225 230 235 240

Lys Ile Met Asp His Arg Asn Ser Leu Thr Phe Pro Pro Glu Val Glu  
245 250 255

Ile Ser Gln Tyr Ala Arg Ser Leu Ile Gln Gly Phe Leu Thr Asp Arg  
260 265 270

Thr Gln Arg Leu Gly Arg Asn Glu Val Glu Glu Ile Lys Arg His Pro  
275 280 285

Phe Phe Ile Asn Asp Gln Trp Thr Phe Asp Asn Leu Arg Asp Ser Ala  
290 295 300

Pro Pro Val Val Pro Glu Leu Ser Gly Asp Asp Asp Thr Arg Asn Phe  
305 310 315 320

Asp Asp Ile Glu Arg Asp Glu Thr Pro Glu Glu Asn Phe Pro Ile Pro  
325 330 335

Lys Thr Phe Ala Gly Asn His Leu Pro Phe Val Gly Phe Thr Tyr Asn  
340 345 350

Gly Asp Tyr Gln Leu Leu Thr Asn Gly Gly Val Arg Asn Ser Asp Met  
355 360 365

Val Asp Thr Lys Leu Asn Asn Ile Cys Val Ser Ser Lys Asp Asp Val  
370 375 380

Leu Asn Leu Gln Asn Leu Leu Glu Gln Glu Lys Gly Asn Ser Glu Asn  
385 390 395 400

Leu Lys Thr Asn Thr Gln Leu Leu Ser Asn Lys Leu Asp Glu Leu Gly

405

410

415

Gln Arg Glu Cys Glu Leu Arg Asn Gln Ala Gly Asp Tyr Glu Lys Glu  
 420. 425 430

Leu Thr Lys Phe Lys Leu Ser Cys Lys Glu Leu Gln Arg Lys Ala Glu  
 435 440 445

Phe Glu Asn Glu Leu Arg Arg Lys Thr Glu Ser Leu Leu Val Glu Thr  
 450 455 460

Lys Lys Arg Leu Asp Glu Glu Gln Asn Lys Arg Thr Arg Glu Met Asn  
 465 470 475 480

Asn Asn Gln Gln His Asn Asp Lys Ile Asn Met Leu Glu Lys Gln Ile  
 485 490 495

Asn Asp Leu Gln Glu Lys Leu Lys Gly Glu Leu Glu His Asn Gln Lys  
 500 505 510

Leu Lys Lys Gln Ala Val Glu Leu Arg Val Ala Gln Ser Ala Thr Glu  
 515 520 525

Gln Leu Asn Asn Glu Leu Gln Glu Thr Met Gln Gly Leu Gln Thr Gln  
 530 535 540

Arg Asp Ala Leu Gln Glu Val Ala Ser Leu Gln Gly Lys Leu Ser  
 545 550 555 560

Gln Glu Arg Ser Ser Arg Ser Gln Ala Ser Asp Met Gln Ile Glu Leu  
 565 570 575

Glu Ala Lys Leu Gln Ala Leu His Ile Glu Leu Glu His Val Arg Asn  
 580 585 590

Cys Glu Asp Lys Val Thr Gln Asp Asn Arg Gln Leu Leu Glu Arg Ile  
 595 600 605

Ser Thr Leu Glu Lys Glu Cys Ala Ser Leu Glu Leu Glu Leu Lys Ala  
 610 615 620

Thr Gln Asn Lys Tyr Glu Gln Glu Val Lys Ala His Arg Glu Thr Glu  
 625 630 635 640

Lys Ser Arg Leu Val Ser Lys Glu Glu Ala Asn Met Glu Glu Val Lys  
 645 650 655

Ala Leu Gln Ile Lys Leu Asn Glu Glu Lys Ser Ala Arg Gln Lys Ser  
 660 665 670

Asp Gln Asn Ser Gln Glu Lys Glu Arg Gln Ile Ser Met Leu Ser Val  
 675 680 685

Asp Tyr Arg Gln Ile Gln Gln Arg Leu Gln Lys Leu Glu Gly Glu Tyr  
 690 695 700

Arg Gln Glu Ser Glu Lys Val Lys Ala Leu His Ser Gln Ile Glu Gln  
 705 710 715 720

Glu Gln Leu Lys Lys Ser Gln Leu Gln Ser Glu Leu Gly Val Gln Arg  
 725 730 735  
 Ser Gln Thr Ala His Leu Thr Ala Arg Glu Ala Gln Leu Val Gly Glu  
 740 745 750  
 Val Ala His Leu Arg Asp Ala Lys Arg Asn Val Glu Glu Leu His  
 755 760 765  
 Lys Leu Lys Thr Ala Arg Ser Val Asp Asn Ala Gln Met Lys Glu Leu  
 770 775 780  
 Gln Glu Gln Val Glu Ala Glu Gln Val Phe Ser Thr Leu Tyr Lys Thr  
 785 790 795 800  
 His Ser Asn Glu Leu Lys Glu Glu Leu Glu Lys Ser Arg His Ile  
 805 810 815  
 Gln Glu Met Glu Glu Glu Arg Glu Ser Leu Val His Gln Leu Gln Ile  
 820 825 830  
 Ala Leu Ala Arg Ala Asp Ser Glu Ala Leu Ala Arg Ser Ile Ala Asp  
 835 840 845  
 Glu Ser Ile Ala Asp Leu Glu Lys Glu Lys Thr Met Lys Glu Leu Glu  
 850 855 860  
 Leu Lys Glu Leu Leu Asn Lys Asn Arg Thr Glu Leu Ser Gln Lys Asp  
 865 870 875 880  
 Ile Ser Ile Ser Ala Leu Arg Glu Arg Glu Asn Glu Gln Lys Lys Leu  
 885 890 895  
 Leu Glu Gln Ile  
 900

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 414 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..414

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GA GCT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA  
 Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly  
 1 5 10 15

AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr 20 25 30	95
GAT GAG AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG AAT GGA AAT GTG Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val 35 40 45	143
ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT GAT GAG Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu 50 55 60	191
AAT GGA AAT GTG ATT AGC ATT ACT GAT GAG AAT GGA AAT GTG ATT AGC Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser 65 70 75	239
ATT ACT GAT GAA AAT GGA AAC TCG AAT AGC ACT ACT AGT GTT TTC AAT Ile Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn 80 85 90 95	287
GAA ACT GAA AAT ATG ACT GGT GCT GCT GAT ACA AAT GAA TAT TCA ATT Glu Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile 100 105 110	335
GGT TCT ACT GAC GGA AAT GGA AAT TTT ATA AGT ACT TTT AGT GAT CAT Gly Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His 115 120 125	383
GAT TAC GTA AGT AAT ACT GAA GAA AAT GAA A Asp Tyr Val Ser Asn Thr Glu Glu Asn Glu 130 135	414

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn 1 5 10 15	
Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp 20 25 30	
Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile 35 40 45	
Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp Glu Asn 50 55 60	
Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Val Ile Ser Ile	

65

70

75

80

Thr Asp Glu Asn Gly Asn Ser Asn Ser Thr Thr Ser Val Phe Asn Glu  
 85 90 95

Thr Glu Asn Met Thr Gly Ala Ala Asp Thr Asn Glu Tyr Ser Ile Gly  
 100 105 110

Ser Thr Asp Gly Asn Gly Asn Phe Ile Ser Thr Phe Ser Asp His Asp  
 115 120 125

Tyr Val Ser Asn Thr Glu Glu Asn Glu  
 130 135

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..273

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AT GAG AAT GGA AAT GTG ATT AGC TAT ACT GAT GAA AAT GGA AAC ATT 47  
 Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile  
 1 5 10 15

ATC AGT ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA 95  
 Ile Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu  
 20 25 30

AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATC AGT 143  
 Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser  
 35 40 45

ACT ACT GAT GAG AAT GGA AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA 191  
 Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly  
 50 55 60

AAT GTG ATT AGC ATT ACT GAT GAA AAT GGA AAC ATT ATT AGT ACT ACT 239  
 Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr  
 65 70 75

GAT GAG AAT GGA AAT GTG ATT AGC AAT ACT CGA G 273  
 Asp Glu Asn Gly Asn Val Ile Ser Asn Thr Arg  
 80 85 90

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu Asn Gly Asn Val Ile Ser Tyr Thr Asp Glu Asn Gly Asn Ile Ile  
 1 5 10 15

Ser Thr Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn  
 20 25 30

Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr  
 35 40 45

Thr Asp Glu Asn Gly Asn Val Ile Ser Ile Thr Asp Glu Asn Gly Asn  
 50 55 60

Val Ile Ser Ile Thr Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Asp  
 65 70 75 80

Glu Asn Gly Asn Val Ile Ser Asn Thr Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 24..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGAAACCCG ACATTCTCAA AAT ATG GAA CCT CAA TCG CTG TCT TGG CAA 50  
 Met Glu Pro Gln Ser Leu Ser Trp Gln  
 1 5

CTT CCG ACT CAA GTA GTT CAG CCA GTT TTT GAA CAA CAA ATG CAG ATT 98  
 Leu Pro Thr Gln Val Val Gln Pro Val Phe Glu Gln Gln Met Gln Ile  
 10 15 20 25

CCT GGA TAT AAT ATG CAA ATT CAA TCT AAT TAT TAT CAA ATT CAC CCA 146  
 Pro Gly Tyr Asn Met Gln Ile Gln Ser Asn Tyr Tyr Gln Ile His Pro  
 30 35 40

GAA ATG TTG GAT CCA AAT TTG AAC AAT CCT CAG CAG TTA ATG TTT AAT 194  
 Glu Met Leu Asp Pro Asn Leu Asn Asn Pro Gln Gln Leu Met Phe Asn

## 2618-17-C4-PUS-2.txt

45

50

55

TAT ATG CAA TTA CAA CAA TTG CAG GAA CTA CAA CAT TTA AGT CAA CAA	242
Tyr Met Gln Leu Gln Gln Leu Glu Leu Gln His Leu Ser Gln Gln	
60 65 70	
CAG CCA ATG CAT CAT GAA TTT GAA CAT CAT ATC CCC ATT CCA CAA GAA	290
Gln Pro Met His His Glu Phe Glu His His Ile Pro Ile Pro Gln Glu	
75 80 85	
GCA ACT TCA ACT AAT TAC GGT CCA TCC GGA CAG TAT ATT ACT AGT GAC	338
Ala Thr Ser Thr Asn Tyr Gly Pro Ser Gly Gln Tyr Ile Thr Ser Asp	
90 95 100 105	
GCA ACA TCT TAT CAA TCA ATT GCC CAA CAA TTT GTA CCA CAA CCA CCA	386
Ala Thr Ser Tyr Gln Ser Ile Ala Gln Gln Phe Val Pro Gln Pro Pro	
110 115 120	
ATT GAA ACT ACC ACC ACG AAA ATA CCT GAA ACT GAA ATT CAA ATT GGC	434
Ile Glu Thr Thr Thr Lys Ile Pro Glu Thr Glu Ile Gln Ile Gly	
125 130 135	
GTT TCG AAT CAA TAT GCC CAA AAT ATA ACT TAT AAT TCA AAT ATC AGT	482
Val Ser Asn Gln Tyr Ala Gln Asn Ile Thr Tyr Asn Ser Asn Ile Ser	
140 145 150	
CCT GAA GTG ATT GGA TTC CGA GAA CAT TAT GTT GCG GAA CAG CCT TCT	530
Pro Glu Val Ile Gly Phe Arg Glu His Tyr Val Ala Glu Gln Pro Ser	
155 160 165	
GGT GAC GTG CTT CAC AAA AGT CAT TTA ACA GAA CAA CCA GCA GAT AAA	578
Gly Asp Val Leu His Lys Ser His Leu Thr Glu Gln Pro Ala Asp Lys	
170 175 180 185	
AGC ACA CGT GGT GAT CAG GAA CCT GTT AGT GAG ACA GGC TCT GGT TTT	626
Ser Thr Arg Gly Asp Gln Glu Pro Val Ser Glu Thr Gly Ser Gly Phe	
190 195 200	
TCG TAT GCA CAA ATT TTA TCA CAG GGA CTT AAG CCT ACC CAG CCA TCC	674
Ser Tyr Ala Gln Ile Leu Ser Gln Gly Leu Lys Pro Thr Gln Pro Ser	
205 210 215	
AAC TCA GTT AAT TTG CTT GCA GAT CGA TCG AGA TCA CCT CTA GAT ACG	722
Asn Ser Val Asn Leu Ala Asp Arg Ser Arg Ser Pro Leu Asp Thr	
220 225 230	
AAA ACG AAA GAA AAT TAT AAA TCT CCT GGT CGT GTG CAG GAT ATC ACG	770
Lys Thr Lys Glu Asn Tyr Lys Ser Pro Gly Arg Val Gln Asp Ile Thr	
235 240 245	
AAA ATA ATA GAT GAG AAA CAA AAG TCG TCA AAA GAC ACA GAG TGG CAT	818
Lys Ile Ile Asp Glu Lys Gln Lys Ser Ser Lys Asp Thr Glu Trp His	
250 255 260 265	
AAT AAG AAA GTG AAA GAA CAT AAA AAA GTG AAA GAT ATC AAA CCT GAT	866
Asn Lys Lys Val Lys Glu His Lys Lys Val Lys Asp Ile Lys Pro Asp	
270 275 280	

## 2618-17-C4-PUS-2.txt

TTC GAA TCT TCT CAA AGG AAT AAG AAA AGC AAG AAT ATT CCT AAG CAA Phe Glu Ser Ser Gln Arg Asn Lys Lys Ser Lys Asn Ile Pro Lys Gln 285 290 295	914
ATT GAA AAT ATC ACA CCT CAA CTT GAC AGC TTA CGA TCA CGA GAT ATA Ile Glu Asn Ile Thr Pro Gln Leu Asp Ser Leu Arg Ser Arg Asp Ile 300 305 310	962
GTA ATT AAG GGA GAA TTA CTA ACA AAA GAT ACT ACA AAA AGT TTA ACT Val Ile Lys Gly Glu Leu Leu Thr Lys Asp Thr Thr Lys Ser Leu Thr 315 320 325	1010
ACT GTT AAT GTT GAT AGT GAA TTA GAT AGT GTA AAA CCT AAA GAT GAA Thr Val Asn Val Asp Ser Glu Leu Asp Ser Val Lys Pro Lys Asp Glu 330 335 340 345	1058
AAA CCT GAA CCT TCT GAA CCT AGT AAA ACG TTT ATT GAT ACT TCA GTT Lys Pro Glu Pro Ser Glu Pro Ser Lys Thr Phe Ile Asp Thr Ser Val 350 355 360	1106
GCA AAG GAT GTT GAT AAT TCT ACA CAG GCG AAC CAT AAA AAG AAG AAA Ala Lys Asp Val Asp Asn Ser Thr Gln Ala Asn His Lys Lys Lys Lys 365 370 375	1154
AGT AAA TCT AAG CCG AGG AAA ACG GAA CCG GAA GAT GAA ATT GAA AAA Ser Lys Ser Lys Pro Arg Lys Thr Glu Pro Glu Asp Glu Ile Glu Lys 380 385 390	1202
GCT TTG AAA GAA ATT CAA GCT AGT GAG AAA AAA CTT ACG AAG TCT ATC Ala Leu Lys Glu Ile Gln Ala Ser Glu Lys Lys Leu Thr Lys Ser Ile 395 400 405	1250
GAT AAC ATT GTG AAT AAA TTT AAT ACA CCA CTT GCT AGT GTT AAA GCC Asp Asn Ile Val Asn Lys Phe Asn Thr Pro Leu Ala Ser Val Lys Ala 410 415 420 425	1298
GAT GAT TCC AAT TCT ACC AAG GAT AAT GTA CCA GCA AAG AAG AAA AAA Asp Asp Ser Asn Ser Thr Lys Asp Asn Val Pro Ala Lys Lys Lys Lys 430 435 440	1346
CCT TCG AAG TCA TCT GTT TCT TTA CCT GAG AAT GTA GTA CAA AAT CTA Pro Ser Lys Ser Val Ser Leu Pro Glu Asn Val Val Gln Asn Leu 445 450 455	1394
TTG ATA CTA ACA TAA CTACTAGTAG CGACAAGATT GAAAACATGC CGCAACCGCA Leu Ile Leu Thr 460	1449
ACCAAAAAGA GAAGATTTAC AAGATGCAGC TAAGGAAGTA TTGACTTCAA TAGAGTCAGT AATGATGCAG TCTGTTGAGA CTATTCTAT TACGAAGAAA AGAGTAAATA AGAAAAAGAA TACCACTCAA CAGACGAAGG AATTTGTGGA ACACGAAATA TGCGATACAT CAAAAAAATGA AACTTTAAAAA AATATTGAAA AAGAATCGCA TGAGAATATG GCTATATTGC AAACAAGTCC GAAACCGCCA CTAAG	1509 1569 1629 1689 1704

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Pro Gln Ser Leu Ser Trp Gln Leu Pro Thr Gln Val Val Gln  
 1 5 10 15

Pro Val Phe Glu Gln Gln Met Gln Ile Pro Gly Tyr Asn Met Gln Ile  
 20 25 30

Gln Ser Asn Tyr Tyr Gln Ile His Pro Glu Met Leu Asp Pro Asn Leu  
 35 40 45

Asn Asn Pro Gln Gln Leu Met Phe Asn Tyr Met Gln Leu Gln Gln Leu  
 50 55 60

Gln Glu Leu Gln His Leu Ser Gln Gln Pro Met His His Glu Phe  
 65 70 75 80

Glu His His Ile Pro Ile Pro Gln Glu Ala Thr Ser Thr Asn Tyr Gly  
 85 90 95

Pro Ser Gly Gln Tyr Ile Thr Ser Asp Ala Thr Ser Tyr Gln Ser Ile  
 100 105 110

Ala Gln Gln Phe Val Pro Gln Pro Pro Ile Glu Thr Thr Thr Thr Lys  
 115 120 125

Ile Pro Glu Thr Glu Ile Gln Ile Gly Val Ser Asn Gln Tyr Ala Gln  
 130 135 140

Asn Ile Thr Tyr Asn Ser Asn Ile Ser Pro Glu Val Ile Gly Phe Arg  
 145 150 155 160

Glu His Tyr Val Ala Glu Gln Pro Ser Gly Asp Val Leu His Lys Ser  
 165 170 175

His Leu Thr Glu Gln Pro Ala Asp Lys Ser Thr Arg Gly Asp Gln Glu  
 180 185 190

Pro Val Ser Glu Thr Gly Ser Gly Phe Ser Tyr Ala Gln Ile Leu Ser  
 195 200 205

Gln Gly Leu Lys Pro Thr Gln Pro Ser Asn Ser Val Asn Leu Leu Ala  
 210 215 220

Asp Arg Ser Arg Ser Pro Leu Asp Thr Lys Thr Lys Glu Asn Tyr Lys  
 225 230 235 240

Ser Pro Gly Arg Val Gln Asp Ile Thr Lys Ile Ile Asp Glu Lys Gln  
 245 250 255

Lys Ser Ser Lys Asp Thr Glu Trp His Asn Lys Lys Val Lys Glu His  
 260 265 270  
 Lys Lys Val Lys Asp Ile Lys Pro Asp Phe Glu Ser Ser Gln Arg Asn  
 275 280 285  
 Lys Lys Ser Lys Asn Ile Pro Lys Gln Ile Glu Asn Ile Thr Pro Gln  
 290 295 300  
 Leu Asp Ser Leu Arg Ser Arg Asp Ile Val Ile Lys Gly Glu Leu Leu  
 305 310 315 320  
 Thr Lys Asp Thr Thr Lys Ser Leu Thr Thr Val Asn Val Asp Ser Glu  
 325 330 335  
 Leu Asp Ser Val Lys Pro Lys Asp Glu Lys Pro Glu Pro Ser Glu Pro  
 340 345 350  
 Ser Lys Thr Phe Ile Asp Thr Ser Val Ala Lys Asp Val Asp Asn Ser  
 355 360 365  
 Thr Gln Ala Asn His Lys Lys Lys Ser Lys Ser Lys Pro Arg Lys  
 370 375 380  
 Thr Glu Pro Glu Asp Glu Ile Glu Lys Ala Leu Lys Glu Ile Gln Ala  
 385 390 395 400  
 Ser Glu Lys Lys Leu Thr Lys Ser Ile Asp Asn Ile Val Asn Lys Phe  
 405 410 415  
 Asn Thr Pro Leu Ala Ser Val Lys Ala Asp Asp Ser Asn Ser Thr Lys  
 420 425 430  
 Asp Asn Val Pro Ala Lys Lys Lys Pro Ser Lys Ser Ser Val Ser  
 435 440 445  
 Leu Pro Glu Asn Val Val Gln Asn Leu Leu Ile Leu Thr  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGAACCTC AATCGCTGTC TTGGCAACTT CCGACTCAAG TAGTTCAGCC AGTTTTTGAA	60
CAACAAATGC AGATTCCTGG ATATAATATG CAAATTCAAT CTAATTATTA TCAAATTAC	120
CCAGAAATGT TGGATCCAAA TTTGAACAAT CCTCAGCAGT TAATGTTAA TTATATGCAA	180

2618-17-C4-PUS-2.txt

TTACAACAAT TGCAGGAACT ACAACATTTA AGTCAACAAAC AGCCAATGCA TCATGAATT	240
GAACATCATA TCCCCATTCC ACAAGAAGCA ACTTCAACTA ATTACGGTCC ATCCGGACAG	300
TATATTACTA GTGACGCAAC ATCTTATCAA TCAATTGCC AACAAATTGT ACCACAACCA	360
CCAATTGAAA CTACCACAC GAAAATACCT GAAACTGAAA TTCAAATTGG CGTTTCGAAT	420
CAATATGCC AACAAATATAAC TTATAATTCA AATATCAGTC CTGAAGTGAT TGGATTCCGA	480
GAACATTATG TTGCGGAACA GCCTTCTGGT GACGTGCTTC ACAAAAGTCA TTTAACAGAA	540
CAACCAGCAG ATAAAAGCAC ACGTGGTGAT CAGGAACCTG TTAGTGAGAC AGGCTCTGGT	600
TTTCGTATG CACAAATTTC ATCACAGGGA CTTAACGCTA CCCAGCCATC CAACTCAGTT	660
AATTGCTTG CAGATCGATC GAGATCACCT CTAGATACGA AAACGAAAGA AAATTATAAA	720
TCTCCTGGTC GTGTGCAGGA TATCACGAAA ATAATAGATG AGAAACAAAA GTCGTCAAAA	780
GACACAGAGT GGCATAATAA GAAAGTGAAA GAACATAAAA AAGTGAAAGA TATCAAACCT	840
GATTTCGAAT CTTCTCAAAG GAATAAGAAA AGCAAGAATA TTCCTAACGCA AATTGAAAAT	900
ATCACACCTC AACTTGACAG CTTACGATCA CGAGATATAG TAATTAAGGG AGAATTACTA	960
ACAAAAGATA CTACAAAAAG TTTAACTACT GTTAATGTTG ATAGTGAATT AGATAGTGT	1020
AAACCTAAAG ATGAAAAACC TGAACCTTCT GAACCTAGTA AAACGTTTAT TGATACTTCA	1080
GTTGCAAAGG ATGTTGATAA TTCTACACAG GCGAACCATATA AAAAGAAGAA AAGTAAATCT	1140
AAGCCGAGGA AAACGGAACC GGAAGATGAA ATTGAAAAAG CTTTGAAAGA AATTCAAGCT	1200
AGTGAGAAAA AACCTTACGAA GTCTATCGAT AACATTGTGA ATAAATTAA TACACCACTT	1260
GCTAGTGTAA AAGCCGATGA TTCCAATTCT ACCAAGGATA ATGTACCAGC AAAGAAGAAA	1320
AAACCTTCGA AGTCATCTGT TTCTTACCT GAGAATGTAG TACAAAATCT ATTGATACTA	1380
ACA	1383

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1...1758

(ix) FEATURE:

(A) NAME/KEY: W = A or T  
 (B) LOCATION: 1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTA GAG ATG GCT AAA TTT CTG ACG GAA ACA TTA GAC GAC ATG ACT CTA Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu	1	5	10	15	48
CAA CAC AAA GAT CAC AGA TCA GAA TTG GCT AAA GAG TTT TCA ATT TGG Gln His Lys Asp His Arg Ser Glu Ala Lys Glu Phe Ser Ile Trp	20	25	30		96
TTT ACG AAA ATG AGA CAG TCT GGC GCT CAA GCC AGT AAC GAA GAA ATC Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile	35	40	45		144
ATG AAA TTT TCA AAA TTG TTT GAA GAT GAA ATC ACT CTT GAC TCG CTG Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu	50	55	60		192
GCG AGG CCG CAA CTT GTT GCT TTG TGC AGG GTA CTA GAA ATC AGT ACT Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr	65	70	75	80	240
TTA GGA ACA ACA AAT TTC TTA AGG TTT CAA CTG CGA ATG AAA CTG CGT Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg	85	90	95		288
TCA TTA GCT GCT GAT GAT AAA ATG ATT CAA AAA GAA GGC ATA GTT TCT Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser	100	105	110		336
ATG ACT TAT TCG GAG GTG CAA CAG GCC TGC AGA GCT CGT GGA ATG CGA Met Thr Tyr Ser Glu Val Gln Ala Cys Arg Ala Arg Gly Met Arg	115	120	125		384
GCT TAT GGT ATG CCT GAA CAT AGG TTG AGG AGG CAA TTG GAA GAC TGG Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp	130	135	140		432
ATT AAT TTA AGC TTG AAT GAA AAG GTT CCA CCA TCA TTA TTG CTT TTG Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu	145	150	155	160	480
TCA AGG GCG CTG ATG TTG CCC GAG AAT GTT CCA GTG TCT GAT AAA CTT Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu	165	170	175		528
AAA GCA ACA ATA AAT GCT CTT CCT GAA ACT ATT GTA ACT CAG ACA AAG Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys	180	185	190		576
GCT GCT ATT GGA GAA AGA GAA GGA AAG ATT GAC AAT AAG ACC AAA ATT Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile	195	200	205		624
GAG GTC ATC AAA GAG GAA GAA CGC AAA ATT CGC GAA GAG CGC CAA GAA					672

## 2618-17-C4-PUS-2.txt

Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu		
210	215	220
GCA CGT GAG GAA GAG GAA CAA CGC AAG CAA GCC GAA CTT GCT CTT AAT		720
Ala Arg Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn		
225	230	235
240		
GCC AGT TCT GCA GCA GCT GAG GCC TCT TCA GCT CAG GAA CTT TTG ATA		768
Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile		
245	250	255
GAT ACA GCT CCT GTA ATA GAT GCA GAA AAG ACA CCA AAG GTG GCA ACA		816
Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr		
260	265	270
TCA CCT GTT GAA TCA CCA TTG GCA CCA CCA GAA GTT CTG ATT ATG GGT		864
Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly		
275	280	285
GCT CCT AAA ACA CCT GTT GCA ACC GAA GTG GAT AAG AAT GCT GAT GAG		912
Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu		
290	295	300
GTG GAA TTC ACC AAG AAA GAT CTT GAG GTT GAA GAT GCA TTG GAT		960
Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp		
305	310	315
320		
ACA CTA TCG AAA GAC AAA AAT AAT TTG GTG ATT GAA AAG GAA GTT ATT		1008
Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile		
325	330	335
AAA GAC ATT AAG GAA GAA ATT GCT GAT TAC CAA GAA GAT GTA GAA GAA		1056
Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu		
340	345	350
TTG AAA GAA GCC ATA GTT GCT GAG AAA CCA AAG GAT GAG ATA AAA		1104
Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys		
355	360	365
GAA ACT AAA GGA GCT CAA CGA TTG TTG AAG AWG GTT AAC AAG ATG ATA		1152
Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile		
370	375	380
ACG AAA ATG GAT ACT GTT GTA CAA GAA ATT GAA AGC AAA GAA TCT GAG		1200
Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu		
385	390	395
400		
AAG AAA GCC AAA ACA TTG CCA CTT GAA GCT CCT AGG AGC GCT ACT GAA		1248
Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu		
405	410	415
ACT CAA GAA TTA GAT GTA AGG AAA GAA AGA GGA GAG ATT TTA ATT GAC		1296
Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp		
420	425	430
GAA TTA ATG GAC GCT ATT AAG AAA GTT AAA AAT GTG CCA GAC GAA AAT		1344
Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn		
435	440	445

2618-17-C4-PUS-2.txt

CGC TTG AAA TTA ATT GAG AAC ATT TTG GGC AGG ATC GAT ACT GAC AAA	1392
Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys	
450 455 460	
GAT AGG CAT ATC AAA GTT GAA GAT GTA TTG AAG GTT ATT GAC ATT GTG	1440
Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val	
465 470 475 480	
GAA AAA GAA GAT GGT ATC ATG AGT ACA AAA CAA TTA GAT GAG TTG GTT	1488
Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val	
485 490 495	
CAG CTT TTG AAA AAG GAG GAA GTT ATT GAA TTG GAA GAA AAG AAA GAA	1536
Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu	
500 505 510	
AAG CAA GAG TCT CAA CAG AAA AGT TTT GTA CCA CCA AGT GAA ACT TTG	1584
Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu	
515 520 525	
CAT CTT GAA TCA TCA CAG CAG AAG AGT ACA GTT CCT AGC TCG GGA CAT	1632
His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His	
530 535 540	
GAA GCT AAG GTG TCC GAA GAT GAC TTA AAT GTT AAA AAT AAA AAT TTG	1680
Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu	
545 550 555 560	
GAA GAA TCG ACC AAA ACT GAA TGT GGA GCA ATT GAC GAA GAG CAC AGA	1728
Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg	
565 570 575	
AGA GAG CAT TGC CAG TAC CCA GAC ATT ACA	1758
Arg Glu His Cys Gln Tyr Pro Asp Ile Thr	
580 585	

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 586 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Glu Met Ala Lys Phe Leu Thr Glu Thr Leu Asp Asp Met Thr Leu	
1 5 10 15	
Gln His Lys Asp His Arg Ser Glu Leu Ala Lys Glu Phe Ser Ile Trp	
20 25 30	
Phe Thr Lys Met Arg Gln Ser Gly Ala Gln Ala Ser Asn Glu Glu Ile	
35 40 45	
Met Lys Phe Ser Lys Leu Phe Glu Asp Glu Ile Thr Leu Asp Ser Leu	
50 55 60	

Ala Arg Pro Gln Leu Val Ala Leu Cys Arg Val Leu Glu Ile Ser Thr  
 65 70 75 80  
 Leu Gly Thr Thr Asn Phe Leu Arg Phe Gln Leu Arg Met Lys Leu Arg  
 85 90 95  
 Ser Leu Ala Ala Asp Asp Lys Met Ile Gln Lys Glu Gly Ile Val Ser  
 100 105 110  
 Met Thr Tyr Ser Glu Val Gln Gln Ala Cys Arg Ala Arg Gly Met Arg  
 115 120 125  
 Ala Tyr Gly Met Pro Glu His Arg Leu Arg Arg Gln Leu Glu Asp Trp  
 130 135 140  
 Ile Asn Leu Ser Leu Asn Glu Lys Val Pro Pro Ser Leu Leu Leu Leu  
 145 150 155 160  
 Ser Arg Ala Leu Met Leu Pro Glu Asn Val Pro Val Ser Asp Lys Leu  
 165 170 175  
 Lys Ala Thr Ile Asn Ala Leu Pro Glu Thr Ile Val Thr Gln Thr Lys  
 180 185 190  
 Ala Ala Ile Gly Glu Arg Glu Gly Lys Ile Asp Asn Lys Thr Lys Ile  
 195 200 205  
 Glu Val Ile Lys Glu Glu Glu Arg Lys Ile Arg Glu Glu Arg Gln Glu  
 210 215 220  
 Ala Arg Glu Glu Glu Gln Arg Lys Gln Ala Glu Leu Ala Leu Asn  
 225 230 235 240  
 Ala Ser Ser Ala Ala Ala Glu Ala Ser Ser Ala Gln Glu Leu Leu Ile  
 245 250 255  
 Asp Thr Ala Pro Val Ile Asp Ala Glu Lys Thr Pro Lys Val Ala Thr  
 260 265 270  
 Ser Pro Val Glu Ser Pro Leu Ala Pro Pro Glu Val Leu Ile Met Gly  
 275 280 285  
 Ala Pro Lys Thr Pro Val Ala Thr Glu Val Asp Lys Asn Ala Asp Glu  
 290 295 300  
 Val Glu Phe Thr Lys Lys Asp Leu Glu Val Val Glu Asp Ala Leu Asp  
 305 310 315 320  
 Thr Leu Ser Lys Asp Lys Asn Asn Leu Val Ile Glu Lys Glu Val Ile  
 325 330 335  
 Lys Asp Ile Lys Glu Glu Ile Ala Asp Tyr Gln Glu Asp Val Glu Glu  
 340 345 350  
 Leu Lys Glu Ala Ile Val Ala Ala Glu Lys Pro Lys Asp Glu Ile Lys  
 355 360 365  
 Glu Thr Lys Gly Ala Gln Arg Leu Leu Lys Xaa Val Asn Lys Met Ile

2618-17-C4-PUS-2.txt

370 375 380  
Thr Lys Met Asp Thr Val Val Gln Glu Ile Glu Ser Lys Glu Ser Glu  
385 390 395 400  
Lys Lys Ala Lys Thr Leu Pro Leu Glu Ala Pro Arg Ser Ala Thr Glu  
405 410 415  
Thr Gln Glu Leu Asp Val Arg Lys Glu Arg Gly Glu Ile Leu Ile Asp  
420 425 430  
Glu Leu Met Asp Ala Ile Lys Lys Val Lys Asn Val Pro Asp Glu Asn  
435 440 445  
Arg Leu Lys Leu Ile Glu Asn Ile Leu Gly Arg Ile Asp Thr Asp Lys  
450 455 460  
Asp Arg His Ile Lys Val Glu Asp Val Leu Lys Val Ile Asp Ile Val  
465 470 475 480  
Glu Lys Glu Asp Gly Ile Met Ser Thr Lys Gln Leu Asp Glu Leu Val  
485 490 495  
Gln Leu Leu Lys Lys Glu Glu Val Ile Glu Leu Glu Glu Lys Lys Glu  
500 505 510  
Lys Gln Glu Ser Gln Gln Lys Ser Phe Val Pro Pro Ser Glu Thr Leu  
515 520 525  
His Leu Glu Ser Ser Gln Gln Lys Ser Thr Val Pro Ser Ser Gly His  
530 535 540  
Glu Ala Lys Val Ser Glu Asp Asp Leu Asn Val Lys Asn Lys Asn Leu  
545 550 555 560  
Glu Glu Ser Thr Lys Thr Glu Cys Gly Ala Ile Asp Glu Glu His Arg  
565 570 575  
Arg Glu His Cys Gln Tyr Pro Asp Ile Thr  
580 585

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: cDNA
- xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCC GG GCTGC AGGA ATT CCGG CACGAGATGA GAATGGAAAT GTGATTAGCT ATACTGATGA 60  
AAATGGAAAC ATTATCAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA TTACTGATGA 120

AAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAC ATTATCAGTA CTACTGATGA	180
GAATGGAAAT GTGATTAGCA TTACTGATGA AAATGGAAAT GTGATTAGCA TTACTGATGA	240
AAATGGAAAC ATTATTAGTA CTACTGATGA GAATGGAAAT GTGATTAGCA ATA	293

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTGGAAACAG CTATGACCAT GATTACCCCA AGCTCGAAAG TAAVCCCTC ACTHARAGGG	60
GAACAAAAGT CTGGAGCTCC ACCCGCGGAT GCGGCCGCB TCTAGAACCT AGTGGACTCC	120
CCCGGSGCTG CAGGAATTCTG GGCACGAGCT CCAGCTAGCC ATATACATTC ATCCAAAATG	180
AAGTTGSAAT GTGTCCTACC CGGCAACGGG ATGCCAGAAA TTGTKTCGAA ATKTGTGGAC	240
GAGCACAAGC TTCGTGTCTK TCTATGAAAA ACGTATGGGA GCAGAAGTCG AGGGCCGACA	300
TCCTCGGCGA TGAATGGARA GGTTATGTGC TCCGA	335

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATAGCTTTA ATATTTTAA TTGATGTATT GCTCAATGGT GATTCTGTT TATTAAACTG	60
AGTTACCAAT ATGCTCGCTT CAATAGACAT AGCAAATGAA AGCATTCCGT ATCCTCAAGC	120
GTTACCAAAC TAACATTAAG GAGTTAATAA AATGTTGTTT CCAATAAATA TAATGGGAAA	180
AACATTTAAT ATTTGTTCCA ATTTGTATTT ATTTTTACTA CAATTATATA CAATAAAATA	240
TTTTTATATA TATTTTATAA AGTTTATGAT GCAGGAGAGA AAATAATGTT AAGAATATAG	300
GTAATGTGTA TATATAAAATG TTTGACAAGC ATGTTCTAGT TAAATAATAA ATACAATGTT	360
AAATCTACTT AAAAAAAA AAAAAAAA AAAAAA	396

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAAAGCGAA	GAATGAAAAG	GGGAAACAAA	AAAAGAAAAG	ACGAAGGAGT	GGAGAGATAA	60
AACGGAGGCA	AAGAAGAAAA	TGAGGATGCA	AAAGAAAGGT	AATAAAAGAG	ATGAAAAGAA	120
GGAAAAAGGA	AATAAGAAAG	AAAGAGTGAG	GGAAAAATAA	AGACAGAGGC	GAAGCAAAAA	180
AGGAGGGAGAA	ATAGAGATTA	AAAAAGAAAT	ACAGCGAAGA	AACCAGGAAA	GCGATAAAGA	240
AAAAAAAAGA	AAAAAAAGAGA	GCAGTGAAAA	AAAAAAAAAA	AAAAAA		285

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATTAA	CTAAAYATTG	TGAAAYAAAT	CATTTCAAA	ATGGTSTCCA	AAGTGTGTTGT	60
TGCTCTTGCC	ATCAATGGCT	TTATAGGGGG	CTSCACAAGY	CTTTTTTCGA	ACAAGATGMC	120
GTCTTAGATA	ASATSGTAGA	TRACATCTCT	GRCTSMATAT	GAGAACARCA	TTGSMAGAAT	180
TAGCCAAGGR	TNGCRAAATT	GATATGMTTS	CYGCTGTAAT	TCGAAAAAA		228

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTT CGT GTC AAC CGC TGG GTC AGA CCT GTT ATT GCT ATG CAC CCA ACC	48
Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr	
1 5 10 15	
ATG ACT CTT GCT GAA CGT CTC GGC AAA AAA GCT TTG CGC GAC CAA TAT	96
Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr	
20 25 30	
GCT CCC GTT TGC TCC ATT GGA CAA CGT AAC ATC AAC ACC TTT GAC AAC	144
Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn	
35 40 45	
ATG ACC TTC CCC GCT CAA TTC GGA AAA TGC TGG CAC GCT TTG TTG CAA	192
Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln	
50 55 60	
ACT GTT CCC CAA AAG TAT TCC GAA GAA CGT GAA TAC AGC GAA GAA CAA	240
Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln	
65 70 75 80	
CAA TAC GAC CGT CAA ATG TCC GTC CTC GTT CGT GAA AAC GGC GAA GAA	288
Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu	
85 90 95	
AAA AGA CGT TAT GAT TGT CTT GGG CAA CCG TTA CAA CAA TTG AAT TGC	336
Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys	
100 105 110	
AAT	339
Asn	

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Arg Val Asn Arg Trp Val Arg Pro Val Ile Ala Met His Pro Thr	
1 5 10 15	
Met Thr Leu Ala Glu Arg Leu Gly Lys Lys Ala Leu Arg Asp Gln Tyr	
20 25 30	

Ala Pro Val Cys Ser Ile Gly Gln Arg Asn Ile Asn Thr Phe Asp Asn  
 35 40 45

Met Thr Phe Pro Ala Gln Phe Gly Lys Cys Trp His Ala Leu Leu Gln  
 50 55 60

Thr Val Pro Gln Lys Tyr Ser Glu Glu Arg Glu Tyr Ser Glu Glu Gln  
 65 70 75 80

Gln Tyr Asp Arg Gln Met Ser Val Leu Val Arg Glu Asn Gly Glu Glu  
 85 90 95

Lys Arg Arg Tyr Asp Cys Leu Gly Gln Pro Leu Gln Gln Leu Asn Cys  
 100 105 110

Asn

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCC AGC TCC TCC AGC TCC AGT GAC TCT TCC AGC TCC AGC AGC TCT  
 Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser  
 1 5 10 15

TCC TCT TCC AGC TCC AGC TCC TCT TCT GAA TCT TCC GAA GAA AAA  
 Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys  
 20 25 30

ACC TCC CAC AAA AAA TCC GAA AAG AAG GAA CAC AAA TCC TGC TCC ATC  
 Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile  
 35 40 45

AAG AAG CAA GTA CAA TTC GTA GAA AAA GAC GGT AAA CTC TGC TTC AGC  
 Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser  
 50 55 60

ATC CGT CCC TTG GCC GCT TGC CAA AAA CAC TGC AAA GCC ACT GAA ACC  
 Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr  
 65 70 75 80

ACT CAA ATG GAA GTC GAA GTA TAC TGC CCC TCT GGC AGC CTT GCT GAA  
 Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu  
 85 90 95

CTT TAC AAA CAA AAG ATC CTT AAG GGA GCC AAC CCC GAC TTG AGC GAC 336

Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp	100	105	110	
AAG ACT CCT TCC AGA ATC TTG AAA TTC AAG GTT CCC AAA GCT TGC ACC				384
Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr	115	120	125	
GCT TAC TAAATCTGAA ATAAATTACA TGGATTAGTT CATTCTGAT GTAGTGCAAT				440
Ala Tyr	130			
TAGTCGATA ATAAATTATT CAATGAGCAT TTAAAAAAA AAAAAAAA AAC				493

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser	1	5	10	15	
Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Ser Glu Glu Lys	20	25	30		
Thr Ser His Lys Lys Ser Glu Lys Lys Glu His Lys Ser Cys Ser Ile	35	40	45		
Lys Lys Gln Val Gln Phe Val Glu Lys Asp Gly Lys Leu Cys Phe Ser	50	55	60		
Ile Arg Pro Leu Ala Ala Cys Gln Lys His Cys Lys Ala Thr Glu Thr	65	70	75	80	
Thr Gln Met Glu Val Glu Val Tyr Cys Pro Ser Gly Ser Leu Ala Glu	85	90	95		
Leu Tyr Lys Gln Lys Ile Leu Lys Gly Ala Asn Pro Asp Leu Ser Asp	100	105	110		
Lys Thr Pro Ser Arg Ile Leu Lys Phe Lys Val Pro Lys Ala Cys Thr	115	120	125		
Ala Tyr	130				

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

2618-17-C4-PUS-2.txt  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTAGTGCAT CATTGTAAA CSTTYTGACG GTKGGCGCT GTATWGGTC TGCCTGGAAA	60
TTGCATCGAT GCACTWCCGT GTCGGCGCA WATAGTGCKK TGGSCCCTGT CTGMMTATAG	120
ACATTCAGGG CGCGGSAKT AGCCATGTT ATGGCTCMCA AWMTGCATT ACAGTGGGGT	180
CACATTCAG TCGCATGATT KMTCAARTTA GTATMWGADA TATATTTTTA TCATACTAAG	240
TAGTGAGCDA ATAACACGCG ARWWACRAAC ACCGAATATC TTKAGTTTT GCACAGATAT	300
KTGTAA	306

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCGGATACG TTGCCAATGA CTACGTCAACC ACCAATGTTG TTTCCACTCC AGTTACTGGA	60
TACACCACCG GACATCTTGC TAATGACTAC GTCACCACCA ATGTTGTATC CACTCCAGTT	120
ACTGGATACA CCACCGGACA TCTTGCCAAAT GACTACGTCA CCACCAACGT AGTTTCCGCA	180
CCAGTCACCA CTGGATACAC CACTGGCTAT ACCACCGGTA ATGTCGGATA CACCACCGGA	240
GTTACTGGTT ACACCAACGG AGTTAGTGGA TATACCAATG GACTTAATGG TTATACCACT	300
GGTAGCTATG TCAGCTCCCC AGGATACACT TCTTCTGGAC TTGTCAACGT TTTCTAGATT	360
TATGATTTCG TCTGCCCTCA ATGATGATGA CCACACTTTT TACTTTTTAT GATATTTGGA	420
AAAAATAAAT AACTGGAAGA ATATATAATA ATTTCAAAAT AAAAAAAA AAAAAAAA	480
CTCGAGGGGG	490

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAAAATCGA AAGAAGGCGT AAAACCAAAA TGGGCACAGA AGGATATTG	GGATTTAGT	60
GATGCCGACA TGGAGAGGTT ACTGGATCAA TGGGAAGAAG ATGAAGACCC	CCTTCCAGAA	120
GACGAATTGC CCGAACATCT CAGACCTGAT CCAAAGATCG ACATAAGCAA	CATCGATATG	180
AGCAATCCCB AAAACATACT AAAGGCTTCC AAAAAAGGCA AGACTTTGAT	GGCATTCTGA	240
CAAGTCAGTG GAAATCCAAC ACAAGAAGAA GCCGAAACCA TCACTAAATT	GTGGCAAGGC	300
AGTCTATGGA ATAGTCATAT ACAAGCCGAA AGATATATGG TTAGCGATGA	CAGGGCTATA	360
TTTATGTTA AAGATGGTTC TCAAGCTTGG CCTGCTAAAG ACTTTTAGT	GGAACAAGAA	420
AGGTGTAAAG ATGTTACAAT TGAAAATAAA ATATATCCTG GTAAATATTC	TTCGACTAAA	480
GAAGAATTAT AATATAATAT ATTATAATTA TAATCTATAA AATAGATTG	AAATTCTACA	540
TTCATGATCT ACTATGTATG ATATTAATTT ATTAAAAATA ATGTTTTTC	AAGTAAAAAA	600
AAAAAAAAAA AAAAAA		616

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCGTGCAGG ACAGATATAG GACCGGATTC GTTAATTGAT TTGAGTGAAG	TGGCTTCTGG	60
TGGTTCTGAT ATTGACACAA AATTTTCCAA TTTAAAAATA GATAAAAAGC	CTGTTGCAAC	120
TTCACAACAA GGAATTGATG AATTTGATAT GTTGCACAA TCGAGAAACA	TTCTAGTGA	180
GGGATCAACC AGTGTATGA AGGAAGGACA CGGTTGGAC TTATTATCAA	ATACACATAA	240
AAATGTACCA CCAACAATTG CACAAGCCGG ACAACTTCCA AGGGATTCTG	AGTTTGATGA	300
AATTGCTGCT TGGCTTGATG AAAAGGTTGA AGACAAAGCC CAAGTCCCCG	AAGACAGTAT	360
TACAAGCAGT GAATTTGATA AATTCTGGC AGAACGGCA GCTGTTGCTG	AAACTTTGCC	420
AAATATTCCA CCGACTACAC AAAGTAATCA TTCAAATATT GAAGCAAACG	ATAAA	475

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGGCACGGG	AGGTAGTGAC	AAAAAATAAC	GATAACGGGAC	TCATCCGAGG	CCCCGTAATC	60
GGAATGAGTA	CACTTTAAAT	CCTTTAACGA	GGATCTATT	GAGGGCCAGT	CTGTGTGCCA	120
GCAGCCGCGG	TAATTCCAGC	TCTAATAGCG	TATATTAAAG	TTGTTGCGGT	TAAAAAGCTC	180
GTAGTTGAAT	CTGTGTCCCA	CACTGTYGGT	TCACCGCTCG	CGGTGTTCAA	CTGGCATGTC	240
TGTGGGACGT	CCTACCGGTG	GGCTTAGCCC	GTCAAAAGGC	GGCCCAACTC	AAAAT	295

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTGACTAAC	CCAGGACTCC	TTTATCCTGT	TTGCGCAATG	TCGATAACCA	TCTCACAAATG	60
GTAAATGATT	TATCGGCTAA	ACAGAAGAGT	CCTAAGAAGG	TTGTTAAAGG	TGTTTCTAGA	120
ATACCGACTT	TTAGACCCAA	GGCTATGAAT	GCTGATGTTG	AGAATTTGA	TTCGATGAGG	180
TGCGATGTTT	GGRACAAAGA	CACCAGTGT	GTTATATAAT	TACTAAAGCA	ATCCACATGT	240
AGCTAATTTT	TTTTTTACAA	TTTTATTTGT	AACTATGTGT	ATTTATATGA	ATTCTTGTGG	300
AATATAATTT	TAAGTTTTA	AATGAAATAT	AGATATTATT	CTAAAAAAA	AAAACAAAAA	360
AAAAAAAAAA	AA					372

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGATTGGCA	CGAGAATT	TTAAGCGCAT	TATTTGCAAG	TGTAATTG	TCCTTTAACG	60
-----------	----------	------------	------------	----------	------------	----

CGGAAGTACA AAATCGAAC	TC	ATGATGTAAG TATTCAAAAA ATTGGGTGGC	120
AAGTATCTAT TCAAAGTAAT AACCAACATT TCTGTGGTGG TTCAATCATT GCTAAAGATT			180
GGGTACTGAC TTCTTCTCAA TGCCTCGTGG ACAAAACAAAG TCCACCGAAG GATTTAACTG			240
TTCGTGTTGG AA			252

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 613 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTCCTGCTG TTAATAGTAC TAATGCAGTA ATTGCTGCHA GCTGCTGCAC AGAGGTTTT	60
AAAATGGCAA CAAGTTGTTA CACCCACATG AACAACTACA TGGTATTCAA TGATACCGAT	120
GGGATTTATA CATATACTTA CGAAGCTGAA AGAAAACCTG ACTGTTAGC TTGTTCACAA	180
ATTCCAAAAAA CTATAGAAGT TTCTAACCTT GAAAATATGA CTCTCCAAGA CTTGATTACT	240
TTGTTGTGTG AAGGGGCTGA ATATCAAATG AAGAGCCCAG GTATTGTAGC CTCAATCGAA	300
GGCAAAAACA AAACCTTATA CATGTCAACA GTAGCAAGTA TAGAAGAAAA GACTAAACAG	360
AATCTAACAA AGTCTCTAAA AGAATTAAAT CTAGAAAATG GAATGGAAC	420
GATGTGACGA CACCAACAC AATATTACTT AAATTAAAAT ATAAGAATGT AATTGAAAAC	480
GATGTTGAGA TGACTTGATA TTTACTTAAA AATGTTATCT TACAATAATT GATAATTAT	540
ATTTAATACT TTTGGAACCTT TGTATTTAAT GATAATAAT TATTATAAGA ATTAAAAAAA	600
AAAAAAAAAAA AAA	613

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 538 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TT GAT ATT TGC TCT GTT GAG GGT GCC TTA GGA TTT TTA GTG GAA ATG Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met 1 5 10 15	47
TTA AAA TAT AAG GCC CCA AGT AAA ACT CTA GCT ATT GTA GAG AAT GCT Leu Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala 20 25 30	95
GGT GGA ATA TTA CGA AAT GTA TCT AGT CAT ATA GCC CTT AGA GAG GAC Gly Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp 35 40 45	143
TAC AGA GAA ATA CTT CGA CAT CAT AAT TGC TTA ACA ATA TTA CTA CAA Tyr Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln 50 55 60	191
CAA TTA AAA TCA CCA AGC CTC ATA ATT GTC AGT AAT GCT TGT GGG ACA Gln Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr 65 70 75	239
TTA TGG AAT TTA TCT GCT AGG AAT TCA ACA GAT CAA CAA TTT TTA TGG Leu Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp 80 85 90 95	287
GAG AAT GGT GTC CCT TTA AGA AGT TTG ATA TAT TCT AAG CAT Glu Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His 100 105 110	335
AAA ATG ATA TCT ATG GGA TCA AGT GCA GCT CTC AAA AAT TTG TTA AAT Lys Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn 115 120 125	383
GCA AAA CCT GAG TGC ATC AAT TTC TTA AGT GAT TCT TCT TCT AAA GGA Ala Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Ser Lys Gly 130 135 140	431
GTT CCA AAT CTA ACT ACA TTG GGT GTA AGA AAA CAA AAA TCT CTA CAT Val Pro Asn Leu Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His 145 150 155	479
GAG TTA ATA GAT CAA AAT CTT TCA GAA ACT TGT GAT AAT ATA GAT AGT Glu Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser 160 165 170 175	527
GTG GCC GCT AA Val Ala Ala	538

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 178 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asp Ile Cys Ser Val Glu Gly Ala Leu Gly Phe Leu Val Glu Met Leu  
 1 5 10 15

Lys Tyr Lys Ala Pro Ser Lys Thr Leu Ala Ile Val Glu Asn Ala Gly  
 20 25 30

Gly Ile Leu Arg Asn Val Ser Ser His Ile Ala Leu Arg Glu Asp Tyr  
 35 40 45

Arg Glu Ile Leu Arg His His Asn Cys Leu Thr Ile Leu Leu Gln Gln  
 50 55 60

Leu Lys Ser Pro Ser Leu Ile Ile Val Ser Asn Ala Cys Gly Thr Leu  
 65 70 75 80

Trp Asn Leu Ser Ala Arg Asn Ser Thr Asp Gln Gln Phe Leu Trp Glu  
 85 90 95

Asn Gly Ala Val Pro Leu Leu Arg Ser Leu Ile Tyr Ser Lys His Lys  
 100 105 110

Met Ile Ser Met Gly Ser Ser Ala Ala Leu Lys Asn Leu Leu Asn Ala  
 115 120 125

Lys Pro Glu Cys Ile Asn Phe Leu Ser Asp Ser Ser Lys Gly Val  
 130 135 140

Pro Asn Leu Thr Thr Leu Gly Val Arg Lys Gln Lys Ser Leu His Glu  
 145 150 155 160

Leu Ile Asp Gln Asn Leu Ser Glu Thr Cys Asp Asn Ile Asp Ser Val  
 165 170 175

Ala Ala

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..388

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CTT CTT AAA CAG TTG GAC TCT GGA TTG TTA CTT GTT ACA GGT CCC  
 Val Leu Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly Pro  
 1 5 10 15

48

TTC TTA ATC AAT GCA TGC CCA TTG CGT CGC ATT TCC CAA AAC TAT GTC

96

Phe	Leu	Ile	Asn	Ala	Cys	Pro	Leu	Arg	Arg	Ile	Ser	Gln	Asn	Tyr	Val	
20							25						30			
ATT	GCC	ACC	TCT	ACC	CGA	TTA	GAC	GTT	AGT	GGA	GTT	AAA	TTA	CCA	GAA	144
Ile	Ala	Thr	Ser	Thr	Arg	Leu	Asp	Val	Ser	Gly	Val	Lys	Leu	Pro	Glu	
35							40					45				
CAC	ATC	AAT	GAT	GAT	TAT	TTC	AAA	AGG	CAA	AAG	AAC	AAG	CGT	GCA	AAG	192
His	Ile	Asn	Asp	Asp	Tyr	Phe	Lys	Arg	Gln	Lys	Asn	Lys	Arg	Ala	Lys	
50							55					60				
AAA	GAG	GAA	GGT	GAT	ATT	TTT	GCT	GCC	AAG	AAA	GAG	GCT	TAT	AAA	CCA	240
Lys	Glu	Glu	Gly	Asp	Ile	Phe	Ala	Ala	Lys	Lys	Glu	Ala	Tyr	Lys	Pro	
65							70				75			80		
ACT	GAG	CAA	AGG	AAG	AAT	GAC	CAA	AAG	CTT	GTA	GAC	AAA	ATG	GTT	TTA	288
Thr	Glu	Gln	Arg	Lys	Asn	Asp	Gln	Lys	Leu	Val	Asp	Lys	Met	Val	Leu	
85							90					95				
GGA	GTA	ATC	AAG	AAG	CAC	CCA	GAC	CAC	AAA	CTT	TTG	TAT	ACA	TAT	TTG	336
Gly	Val	Ile	Lys	Lys	His	Pro	Asp	His	Lys	Leu	Leu	Tyr	Thr	Tyr	Leu	
100							105					110				
TCA	GCT	ATG	TTT	GGT	TTG	AAA	TCT	TCC	CAA	TAT	CCA	CAT	CGT	ATG	AAG	384
Ser	Ala	Met	Phe	Gly	Leu	Lys	Ser	Ser	Gln	Tyr	Pro	His	Arg	Met	Lys	
115							120					125				
TTC	T	AAATACTATA	TTCATAAAAT	AAATTGAACT	TCTCAAAAAA	AAAAA										432
Phe																

## (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Val	Leu	Leu	Lys	Gln	Leu	Asp	Ser	Gly	Leu	Leu	Leu	Val	Thr	Gly	Pro	
1					5				10				15			
Phe	Leu	Ile	Asn	Ala	Cys	Pro	Leu	Arg	Arg	Ile	Ser	Gln	Asn	Tyr	Val	
20							25						30			
Ile	Ala	Thr	Ser	Thr	Arg	Leu	Asp	Val	Ser	Gly	Val	Lys	Leu	Pro	Glu	
35							40					45				
His	Ile	Asn	Asp	Asp	Tyr	Phe	Lys	Arg	Gln	Lys	Asn	Lys	Arg	Ala	Lys	
50							55					60				
Lys	Glu	Glu	Gly	Asp	Ile	Phe	Ala	Ala	Lys	Lys	Glu	Ala	Tyr	Lys	Pro	
65							70				75			80		
Thr	Glu	Gln	Arg	Lys	Asn	Asp	Gln	Lys	Leu	Val	Asp	Lys	Met	Val	Leu	

Gly Val Ile Lys Lys His Pro Asp His Lys Leu Leu Tyr Thr Tyr Leu  
 100 105 110

Ser Ala Met Phe Gly Leu Lys Ser Ser Gln Tyr Pro His Arg Met Lys  
 115 120 125

Phe

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 47..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGGAAATTCA ATATTTTGTT TTAACATTAA ATTTTCAAA TTGATG ATG AAA TTT 5 10 15	Met Lys Phe	55
TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG 5 10 15	Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met	103
TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT 20 25 30 35	Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	151
ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT 40 45 50	Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	199
TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT 55 60 65	Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys	247
GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT 70 75 80	Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn	295
CAA AAA CAC TGT TAT TGC GA ATAACCATAT TCCGGATGAA AGACCAAATT 85	Gln Lys His Cys Tyr Cys	345
GATATAAATT ACTAAAATT TGCTAGATAG CAATCATAAA ATTTGAAGT TTTCAATGAT		405

CCTAACATGT TTTGCCTCCA ATTTATTTA ACAGCAAATT GCTGGAACT TACCGTACCG	465
TAACAAAATG TTCAAGAAAT ACTGAATGTT TACAAATAGA TTATTATAAA TATTGTAACA	525
TTGTCTAATA TTTATAAGAA TTATATAAAC TGAATTGCAA AAGTTGAAAA AAAAAAAA	585
AAAAAAA	595

## (2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln			
1	5	10	15
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn			
20	25	30	
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile			
35	40	45	
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys			
50	55	60	
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr			
65	70	75	80
Arg Pro Asn Gln Lys His Cys Tyr Cys			
85			

## (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 595 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTTTTTTTT TTTTTTTTTT TTTTCAACTT TTGCAATTCA GTTTATATAA TTCTTATAAA	60
TATTAGACAA TGTTACAATA TTTATAATAA TCTATTGTA AACATTCAGT ATTTCTTGAA	120
CATTTTGTAA CGGTACGGTA AGTTCCCAGC AATTTGCTGT TAAAATAAAT TGGAGGCAA	180

ACATGTTAGG ATCATTGAAA ACTTCAAAAT TTTATGATTG CTATCTAGCA TAATTTAGT	240
AATTTATATC AATTGGTCT TTCATCCGGA ATATGGTTAT TCGCAATAAC AGTGTTCAG	300
ATTTGGTCGT GTTGAACCAC CGTTCCACA AGCACCACCT CCAAATCCAC ATTGACTTT	360
GCAAAATATT TTGCAACTTT GATGATTCC AATACAAAAA TCTTCAATAG TAAGCTTCCC	420
AGATGGTATT GACACCTCTT TTGTACTTGG ATTATTCCT CCCGATTAC ACTTTTCAGT	480
GACCATTTT GACATAGATA CTTGATTAA TAAAACACAC AACACGAAA TTGCCAGTAA	540
AAATTCATA TCGAATTGAA AAAATTAAAT GTTAAAACAA AATATTGAAT TTCCA	595

## (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA	48
Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln	
1 5 10 15	
GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT	96
Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn	
20 25 30	
AAT CCA AGT ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT	144
Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile	
35 40 45	
GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA	192
Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys	
50 55 60	
AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA	240
Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr	
65 70 75 80	
CGA CCA AAT CAA AAA CAC TGT TAT TGC GAA	270
Arg Pro Asn Gln Lys His Cys Tyr Cys Glu	
85 90	

## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln  
1 5 10 15

Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn  
20 25 30

Asn Pro Ser Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile  
35 40 45

Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys  
50 55 60

Ser Gln Cys Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr  
 65 70 75 80

Arg Pro Asn Gln Lys His Cys Tyr Cys Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCGCAATAA CAGTGTTCG GATTTGGTCG TGTTGAACCA CCGTTCCAC AAGCACCACC 60  
TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA 120  
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC 180  
TCCCGATTTA CACTTTTCAG TGACCATTTC TGACATAGAT ACTTGATTTA ATAAAACACA 240  
CAACACGCCAA ATTGCCAGTA AAAATTTCAT 270

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCA AAA ATG GTC ACT GAA AAG TGT AAA TCG GGA GGA AAT AAT CCA AGT Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	48
1 5 10 15	
ACA AAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	96
20 25 30	
TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TGC AAA AGT CAA TGT Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys	144
35 40 45	
GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT Gly Phe Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn	192
50 55 60	
CAA AAA CAC TGT TAT TGC GAA Gln Lys His Cys Tyr Cys Glu	213
65 70	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser  
 1 5 10 15

Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe  
 20 25 30

Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys  
 35 40 45

Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn  
 50 55 60

Gln Lys His Cys Tyr Cys Glu  
 65 70

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

2618-17-C4-PUS-2.txt

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TTCGCAATAA CAGTGTFFFF GATTTGGTCG TGTTGAACCA CCGTTTCCAC AAGCACCACC	60
TCCAAATCCA CATTGACTTT TGCAAAATAT TTTGCAACTT TGATGATTTC CAATACAAAA	120
ATCTTCAATA GTAAGCTTCC CAGATGGTAT TGACACCTCT TTTGTACTTG GATTATTTCC	180
TCCCGATTAA CACTTTTCAG TGACCATTAA TGA	213

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1007 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGG AAA GTT AAT AAA AAA TGT ACA TCA GGT GGA AAA AAT CAA GAT AGA	48
Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg	
1 5 10 15	
AAA CTC GAT CAA ATA ATT CAA AAA GGC CAA CAA GTT AAA ATC CAA AAT	96
Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn	
20 25 30	
ATT TGC AAA TTA ATA CGA GAT AAA CCA CAT ACA AAT CAA GAG AAA GAA	144
Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu	
35 40 45	
AAA TGT ATG AAA TTT TGC AAA AAA GTT TGC AAA GGT TAT AGA GGA GCT	192
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala	
50 55 60	
TGT GAT GGC AAT ATT TGC TAC TGC AGC AGG CCA AGT AAT TTA GGT CCT	240
Cys Asp Gly Asn Ile Cys Tyr Cys Ser Arg Pro Ser Asn Leu Gly Pro	
65 70 75 80	
GAT TGG AAA GTA AGC AAA GAA TGC AAA GAT CCC AAT AAC AAA GAT TCT	288
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser	
85 90 95	

CGT CCT ACG GAA ATA GTT CCA TAT CGA CAA CAA TTA GCA AAT CCA AAT Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn 100 105 110	336
ATT TGC AAA CTA AAA AAT TCA GAG ACC AAT GAA GAT TCC AAA TGC AAA Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys 115 120 125	384
AAA CAT TGC AAA GAA AAA TGT CGT GGT GGA AAT GAT GCT GGA TGT GAT Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp 130 135 140	432
GGA AAC TTT TGT TAT TGT CGA CCA AAA AAT AAA TAATAATTAT AATAAATAAA Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys 145 150 155	485
TTGTTATAGT TATTAGTTAT CCCATCACAT ATTAGAAAAG TGGCTTATAA TTTATGAACA	545
ATATAACACA TAAATTAGTT GTGTAATTTC GAATGTTTT TTCAAATATA AGGCGTTTT	605
CTAGAATATC TTGATATTAG AAACTAACTT AGATTATTTT GTTGTGTATA AAATATTCAA	665
ATACGTAAGT TATATTGAAC AAAGCATTAA GAAGCTACAT TAGATATACT AAATAAGTGC	725
AAAATTGCAT GGAAACCCTT ACTGGATTAA CTACATATT TCTTCCTAAA TATTGTCTTG	785
GTATTACTCT TATTATATAA AAATTAATAT AAAATTGTAG ACAGAGACGA ATTGGGGTAT	845
TGTTATATAT AAAAAAGTAG TGGATTATTT AATTCTAAAA AAGTTGCAA AATGTTTCAT	905
ACATAATAAC CGAATATTTT CAAATATATA AATATTGTAA TGAATAATG CGCATCTGTA	965
TGCTTAATAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	1007

## (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Trp Lys Val Asn Lys Lys Cys Thr Ser Gly Gly Lys Asn Gln Asp Arg 1 5 10 15
Lys Leu Asp Gln Ile Ile Gln Lys Gly Gln Gln Val Lys Ile Gln Asn 20 25 30
Ile Cys Lys Leu Ile Arg Asp Lys Pro His Thr Asn Gln Glu Lys Glu 35 40 45
Lys Cys Met Lys Phe Cys Lys Lys Val Cys Lys Gly Tyr Arg Gly Ala 50 55 60

Cys	Asp	Gly	Asn	Ile	Cys	Tyr	Cys	Ser	Arg	Pro	Ser	Asn	Leu	Gly	Pro
65					70				75						80
Asp Trp Lys Val Ser Lys Glu Cys Lys Asp Pro Asn Asn Lys Asp Ser															
									85		90				95
Arg Pro Thr Glu Ile Val Pro Tyr Arg Gln Gln Leu Ala Asn Pro Asn															
									100		105				110
Ile Cys Lys Leu Lys Asn Ser Glu Thr Asn Glu Asp Ser Lys Cys Lys															
									115		120				125
Lys His Cys Lys Glu Lys Cys Arg Gly Gly Asn Asp Ala Gly Cys Asp															
									130		135				140
Gly Asn Phe Cys Tyr Cys Arg Pro Lys Asn Lys															
145					150										155

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTATATTAAG	CATACAGATG	CGCATTATT	60
CATTACAATA	TTTATATATT	TGAAAATATT	CGGTTATTAT	GTATGAAACA	TTTGCAAAC	120
TTTTTTAGAA	TTAAATAATC	CACTACTTTT	TTATATATAA	CAATACCCCA	ATTCGTCTCT	180
GTCTACAATT	TTATATTAAT	TTTTATATAA	TAAGAGTAAT	ACCAAGACAA	TATTTAGGAA	240
GAAAATATGT	AGTAAATCCA	GTAAGGGTTT	CCATGCAATT	TTGCACCTAT	TTAGTATATC	300
TAATGTAGCT	TCTAAATGCT	TTGTTCAATA	TAACTTACGT	ATTTGAATAT	TTTATACACA	360
ACAAAATAAT	CTAAGTTAGT	TTCTAATATC	AAGATATTCT	AGAAAAACGC	CTTATATTG	420
AAAAAAACAT	TCGAAATTAC	ACAACTAATT	TATGTGTTAT	ATTGTTCATA	AATTATAAGC	480
CACTTTCTA	ATATGTGATG	GGATAACTAA	TAACTATAAC	AATTTATTAA	TTATAATTAT	540
TATTTATTTT	TTGGTCGACA	ATAACAAAAG	TTTCCATCAC	ATCCAGCATC	ATTTCCACCA	600
CGACATTTTT	CTTGCAATG	TTTTTGCAAT	TTGGAATCTT	CATTGGTCTC	TGAATTTTT	660
AGTTTGCAAA	TATTTGGAAT	TGCTAATTGT	TGTCGATATG	GAACTATTTC	CGTAGGACGA	720
GAATCTTGT	TATTGGGATC	TTTGCATTCT	TTGCTTACTT	TCCAATCAGG	ACCTAAATT	780

CTTGGCCTGC TGCAGTAGCA AATATTGCCA TCACAAGCTC CTCTATAACC TTTGCAAAC	840
TTTTTGCAAA ATTCATACA TTTTCTTTC TCTTGATTTG TATGTGGTTT ATCTCGTATT	900
AATTTGCAAA TATTTGGAT TTTAACCTGT TGGCCTTTT GAATTATTTG ATCGAGTTT	960
CTATCTTGAT TTTTCCACC TGATGTACAT TTTTATTAA CTTTCCA	1007

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1062

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCA GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT ATG TCA CAT ACA	48
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr	
1 5 10 15	
CCT TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG TCT GAA GAT	96
Pro Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp	
20 25 30	
TCA AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA TTA AAA ATT GGC	144
Ser Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly	
35 40 45	
AAA TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA GTT GAC AAA TGG	192
Lys Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp	
50 55 60	
GAT TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT ACG AGA AGA TCT	240
Asp Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Thr Arg Arg Ser	
65 70 75	
CAA GAA GGA GCG CTT ATC ATT GGT TCT GGT CTÀ GAA GAA AAG GAA AAG	288
Gln Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys	
80 85 90 95	
GCA GTT TGG ACA AAA GAG AAA GGA GAT AAA ACC ATA TTT TCT TCG TTT	336
Ala Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe	
100 105 110	
GGT GAA TAT GCT AAA TTT TAT AGT CCA AAA ACT TGT CCA AAC TTC ATA	384
Gly Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile	
115 120 125	
GCA CAA CAG AAA ATA GCA GTA AGA GAC TTG TTA ACA AAA AGT GCA AAA	432
Ala Gln Gln Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys	

## 2618-17-C4-PUS-2.txt

130	135	140	
GAT TAT AAA AAT TCA CTT GCA AAA TTA AAA GAA GCG TAT AAA ATA GAT Asp Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp 145	150	155	480
GCG ACG ACA AGC CCT CAG AAT GTT TGG CTG GCA TAT GAA ACT TTG AAT Ala Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn 160	165	170	528
TTA CAA AGC AAG CAA AAT AAC GCT CCA ACA TGG TGG AAT ACT GTA AAC Leu Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn 180	185	190	576
AAA GAT CTA AAA CAA TTC TCT GAG AAA TAT TTA TGG ACC GCC TTG ACT Lys Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr 195	200	205	624
TCT AAT GAT AAT CTT AGA AAG ATG TCA GGA GGT CGT ATG ATT AAC GAT Ser Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp 210	215	220	672
ATA TTG AAC GAT ATC GAA AAC ATA AAG AAA GGA GAG GGA CAA CCG GGT Ile Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly 225	230	235	720
GCT CCA GGA GGA AAG GAA AAC AAA TTA TCA GTG CTG ACC GTT CCT CAA Ala Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln 240	245	250	768
GCT ATC TTA GCA GCA TTT GTT TCA GCA TTT GCT CCC GAA GGT ACA AAA Ala Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys 260	265	270	816
ATT GAA AAT AAG GAC CTT GAT CCG TCT ACT TTA TAT CCT GGC CAA GGA Ile Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly 275	280	285	864
GCA CTT CAC GTT ATT GAA CTA CAC CAA GAT AAG AGC GAT TGG AGC ATA Ala Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile 290	295	300	912
AAA GTT CTC TAT AGA AAC AAT GAC CAA ATG AAG CTG AAA CCA ATG AAA Lys Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys 305	310	315	960
CTT GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG Leu Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met 320	325	330	1008
CTA CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA Leu Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys 340	345	350	1056
ACG TCG TAAAAATTAA AAATAAAAAC TTTTCAATAT ATTTTCCGCT AAAATAAATA Thr Ser			1112
AATATGTTG TATATTAAA CTTATCAAAA TAATAGTAGT GTTTAATAA AGATTTAAA			1172

TAAATAATTG TAAAAAAAAA AAAAAAAA AAA

1205

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Glu	Leu	Lys	Phe	Val	Phe	Ala	Thr	Ala	Arg	Gly	Met	Ser	His	Thr	Pro
1				5				10						15	
Cys	Asp	Tyr	Pro	Gly	Gly	Pro	Lys	Ile	Thr	His	Lys	Ser	Glu	Asp	Ser
					20			25					30		
Ser	Gln	Leu	Thr	Pro	Ala	Gly	Gln	Glu	Glu	Ala	Leu	Lys	Ile	Gly	Lys
	35					40						45			
Leu	Leu	Ser	Glu	His	Tyr	Arg	Thr	Asn	Leu	Lys	Val	Asp	Lys	Trp	Asp
					50		55				60				
Ser	Asn	Lys	Asn	Tyr	Trp	Thr	Leu	Ala	Ser	Ala	Thr	Arg	Arg	Ser	Gln
	65				70			75				80			
Glu	Gly	Ala	Leu	Ile	Ile	Gly	Ser	Gly	Leu	Glu	Glu	Lys	Glu	Lys	Ala
					85			90				95			
Val	Trp	Thr	Lys	Glu	Lys	Gly	Asp	Lys	Thr	Ile	Phe	Ser	Ser	Phe	Gly
					100		105				110				
Glu	Tyr	Ala	Lys	Phe	Tyr	Ser	Pro	Lys	Thr	Cys	Pro	Asn	Phe	Ile	Ala
			115			120				125					
Gln	Gln	Lys	Ile	Ala	Val	Arg	Asp	Leu	Leu	Thr	Lys	Ser	Ala	Lys	Asp
	130				135					140					
Tyr	Lys	Asn	Ser	Leu	Ala	Lys	Leu	Lys	Glu	Ala	Tyr	Lys	Ile	Asp	Ala
	145				150				155			160			
Thr	Thr	Ser	Pro	Gln	Asn	Val	Trp	Leu	Ala	Tyr	Glu	Thr	Leu	Asn	Leu
					165			170			175				
Gln	Ser	Lys	Gln	Asn	Asn	Ala	Pro	Thr	Trp	Trp	Asn	Thr	Val	Asn	Lys
					180			185			190				
Asp	Leu	Lys	Gln	Phe	Ser	Glu	Lys	Tyr	Leu	Trp	Thr	Ala	Leu	Thr	Ser
					195		200				205				
Asn	Asp	Asn	Leu	Arg	Lys	Met	Ser	Gly	Gly	Arg	Met	Ile	Asn	Asp	Ile
					210		215				220				
Leu	Asn	Asp	Ile	Glu	Asn	Ile	Lys	Lys	Gly	Glu	Gly	Gln	Pro	Gly	Ala

225	230	235	240
Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala			
245	250	255	
Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile			
260	265	270	
Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala			
275	280	285	
Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys			
290	295	300	
Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu			
305	310	315	320
Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu			
325	330	335	
Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr			
340	345	350	

Ser

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TTTTTTTTTT TTTTTTTTT TTACAATTAT TTATTTAAAA TCTTTATTAA AACACTACTA	60
TTATTTTGAT AAGTTTAAAT ATACAAACAT ATTTATTTAT TTTAGCGGAA AATATATTGA	120
AAAGTTTTTA TTTTAATT TTACGACGTT TTACATAATT TATCATGAGC TTCTTCTCC	180
ATGTTATATT TTTGTAGCAT TGATTTGAAA GTACCATAAG AACACTTGTC ACCGCATTGT	240
GCAAGTTCA TTGGTTTCAG CTTCATTTGG TCATTGTTTC TATAGAGAAC TTTTATGCTC	300
CAATCGCTCT TATCTTGGTG TAGTTCAATA ACGTGAAGTG CTCCTTGGCC AGGATATAAA	360
GTAGACGGAT CAAGGTCCCTT ATTTCAATT TTTGTACCTT CGGGAGCAAA TGCTGAAACA	420
AATGCTGCTA AGATAGCTTG AGGAACGGTC AGCACTGATA ATTTGTTTTC CTTTCCTCCT	480
GGAGCACCCG GTTGTCCCTC TCCTTTCTTT ATGTTTTCGA TATCGTTCAA TATATCGTTA	540
ATCATAACGAC CTCCTGACAT CTTTCTAAGA TTATCATTAG AAGTCAAGGC GGTCCATAAA	600
TATTTCTCAG AGAATTGTTT TAGATCTTG TTTACAGTAT TCCACCATGT TGGAGCGTTA	660

TTTGCTTGC	TTTGTAAATT	CAAAGTTCA	TATGCCAGCC	AAACATTCTG	AGGGCTTGT	720
GTCGCATCTA	TTTTATACGC	TTCTTTAAT	TTTGCAGTG	AATTTTATA	ATCTTTGCA	780
CTTTTGT	ACAAGTCTCT	TACTGCTATT	TTCTGTTGT	CTATGAAGTT	TGGACAAGTT	840
TTGGACTAT	AAAATTAGC	ATATTACCA	AACGAAGAAA	ATATGGTTT	ATCTCCTTC	900
TCTTTGTCC	AAACTGCCTT	TTCCTTTCT	TCTAGACCAG	AACCAATGAT	AAGCGCTCCT	960
TCTTGAGATC	TTCTCGTAGC	ACTAGCTAAT	GTCCAATAAT	TTTTATTTGA	ATCCCATTG	1020
TCAACTTTA	AATTAGTTCT	GTAATGTTCG	GATAATAATT	TGCCAATT	TAATGCCTCT	1080
TCTTGACCTG	CCGGTGTCAA	TTGGCTTGAA	TCTTCAGACT	TGTGTGTAAT	TTTTGGACCG	1140
CCTGGATAAT	CACAAGGTGT	ATGTGACATA	CCTCGTGCAG	TCGCAAACAC	AAATTCAAT	1200
TCTGC						1205

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1059

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAA TTG AAA TTT GTG TTT GCG ACT GCA CGA GGT	ATG TCA CAT ACA CCT	48	
Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly	Met Ser His Thr Pro		
1	5	10	15
TGT GAT TAT CCA GGC GGT CCA AAA ATT ACA CAC AAG	TCT GAA GAT TCA	96	
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys	Ser Glu Asp Ser		
20	25	30	
AGC CAA TTG ACA CCG GCA GGT CAA GAA GAG GCA	TTA AAA ATT GGC AAA	144	
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala	Leu Lys Ile Gly Lys		
35	40	45	
TTA TTA TCC GAA CAT TAC AGA ACT AAT TTA AAA	GTT GAC AAA TGG GAT	192	
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys	Val Asp Lys Trp Asp		
50	55	60	
TCA AAT AAA AAT TAT TGG ACA TTA GCT AGT GCT	ACG AGA AGA TCT CAA	240	
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala	Thr Arg Arg Ser Gln		
65	70	75	80
GAA GGA GCG CTT ATC ATT GGT TCT GGT CTA GAA	GAA AAG GAA AAG GCA	288	

Glu	Gly	Ala	Leu	Ile	Ile	Gly	Ser	Gly	Leu	Glu	Glu	Lys	Glu	Lys	Ala	
85									90					95		
GTT	TGG	ACA	AAA	GAG	AAA	GGA	GAT	AAA	ACC	ATA	TTT	TCT	TCG	TTT	GGT	336
Val	Trp	Thr	Lys	Glu	Lys	Gly	Asp	Lys	Thr	Ile	Phe	Ser	Ser	Phe	Gly	
100								105					110			
GAA	TAT	GCT	AAA	TTT	TAT	AGT	CCA	AAA	ACT	TGT	CCA	AAC	TTC	ATA	GCA	384
Glu	Tyr	Ala	Lys	Phe	Tyr	Ser	Pro	Lys	Thr	Cys	Pro	Asn	Phe	Ile	Ala	
115								120					125			
CAA	CAG	AAA	ATA	GCA	GTA	AGA	GAC	TTG	TTA	ACA	AAA	AGT	GCA	AAA	GAT	432
Gln	Gln	Lys	Ile	Ala	Val	Arg	Asp	Leu	Leu	Thr	Lys	Ser	Ala	Lys	Asp	
130							135					140				
TAT	AAA	AAT	TCA	CTT	GCA	AAA	TTA	AAA	GAA	GCG	TAT	AAA	ATA	GAT	GCG	480
Tyr	Lys	Asn	Ser	Leu	Ala	Lys	Leu	Lys	Glu	Ala	Tyr	Lys	Ile	Asp	Ala	
145						150				155			160			
ACG	ACA	AGC	CCT	CAG	AAT	GTT	TGG	CTG	GCA	TAT	GAA	ACT	TTG	AAT	TTA	528
Thr	Thr	Ser	Pro	Gln	Asn	Val	Trp	Leu	Ala	Tyr	Glu	Thr	Leu	Asn	Leu	
165							170					175				
CAA	AGC	AAG	CAA	AAT	AAC	GCT	CCA	ACA	TGG	TGG	AAT	ACT	GTA	AAC	AAA	576
Gln	Ser	Lys	Gln	Asn	Asn	Ala	Pro	Thr	Trp	Trp	Asn	Thr	Val	Asn	Lys	
180							185					190				
GAT	CTA	AAA	CAA	TTC	TCT	GAG	AAA	TAT	TTA	TGG	ACC	GCC	TTG	ACT	TCT	624
Asp	Leu	Lys	Gln	Phe	Ser	Glu	Lys	Tyr	Leu	Trp	Thr	Ala	Leu	Thr	Ser	
195						200					205					
AAT	GAT	AAT	CTT	AGA	AAG	ATG	TCA	GGA	GGT	CGT	ATG	ATT	AAC	GAT	ATA	672
Asn	Asp	Asn	Leu	Arg	Lys	Met	Ser	Gly	Gly	Arg	Met	Ile	Asn	Asp	Ile	
210						215					220					
TTG	AAC	GAT	ATC	GAA	AAC	ATA	AAG	AAA	GGA	GAG	GGA	CAA	CCG	GGT	GCT	720
Leu	Asn	Asp	Ile	Glu	Asn	Ile	Lys	Lys	Gly	Glu	Gly	Gln	Pro	Gly	Ala	
225						230				235			240			
CCA	GGA	GGA	AAG	GAA	AAC	AAA	TTA	TCA	GTG	CTG	ACC	GTT	CCT	CAA	GCT	768
Pro	Gly	Gly	Lys	Glu	Asn	Lys	Leu	Ser	Val	Leu	Thr	Val	Pro	Gln	Ala	
245							250					255				
ATC	TTA	GCA	GCA	TTT	GTT	TCA	GCA	TTT	GCT	CCC	GAA	GGT	ACA	AAA	ATT	816
Ile	Leu	Ala	Ala	Phe	Val	Ser	Ala	Phe	Ala	Pro	Glu	Gly	Thr	Lys	Ile	
260						265					270					
GAA	AAT	AAG	GAC	CTT	GAT	CCG	TCT	ACT	TTA	TAT	CCT	GGC	CAA	GGA	GCA	864
Glu	Asn	Lys	Asp	Leu	Asp	Pro	Ser	Thr	Leu	Tyr	Pro	Gly	Gln	Gly	Ala	
275						280					285					
CTT	CAC	GTT	ATT	GAA	CTA	CAC	CAA	GAT	AAG	AGC	GAT	TGG	AGC	ATA	AAA	912
Leu	His	Val	Ile	Glu	Leu	His	Gln	Asp	Lys	Ser	Asp	Trp	Ser	Ile	Lys	
290						295					300					
GTT	CTC	TAT	AGA	AAC	AAT	GAC	CAA	ATG	AAG	CTG	AAA	CCA	ATG	AAA	CTT	960
Val	Leu	Tyr	Arg	Asn	Asn	Asp	Gln	Met	Lys	Leu	Lys	Pro	Met	Lys	Leu	
305						310				315			320			

GCA CAA TGC GGT GAC AAG TGT TCT TAT GGT ACT TTC AAA TCA ATG CTA Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu 325 330 335	1008
CAA AAA TAT AAC ATG GAG AAG GAA GCT CAT GAT AAA TTA TGT AAA ACG Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr 340 345 350	1056
TCG Ser	1059

## (2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 353 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Leu Lys Phe Val Phe Ala Thr Ala Arg Gly Met Ser His Thr Pro 1 5 10 15
Cys Asp Tyr Pro Gly Gly Pro Lys Ile Thr His Lys Ser Glu Asp Ser 20 25 30
Ser Gln Leu Thr Pro Ala Gly Gln Glu Glu Ala Leu Lys Ile Gly Lys 35 40 45
Leu Leu Ser Glu His Tyr Arg Thr Asn Leu Lys Val Asp Lys Trp Asp 50 55 60
Ser Asn Lys Asn Tyr Trp Thr Leu Ala Ser Ala Thr Arg Arg Ser Gln 65 70 75 80
Glu Gly Ala Leu Ile Ile Gly Ser Gly Leu Glu Glu Lys Glu Lys Ala 85 90 95
Val Trp Thr Lys Glu Lys Gly Asp Lys Thr Ile Phe Ser Ser Phe Gly 100 105 110
Glu Tyr Ala Lys Phe Tyr Ser Pro Lys Thr Cys Pro Asn Phe Ile Ala 115 120 125
Gln Gln Lys Ile Ala Val Arg Asp Leu Leu Thr Lys Ser Ala Lys Asp 130 135 140
Tyr Lys Asn Ser Leu Ala Lys Leu Lys Glu Ala Tyr Lys Ile Asp Ala 145 150 155 160
Thr Thr Ser Pro Gln Asn Val Trp Leu Ala Tyr Glu Thr Leu Asn Leu 165 170 175
Gln Ser Lys Gln Asn Asn Ala Pro Thr Trp Trp Asn Thr Val Asn Lys 180 185 190

2618-17-C4-PUS-2.txt

Asp Leu Lys Gln Phe Ser Glu Lys Tyr Leu Trp Thr Ala Leu Thr Ser  
195 200 205

Asn Asp Asn Leu Arg Lys Met Ser Gly Gly Arg Met Ile Asn Asp Ile  
210 215 220

Leu Asn Asp Ile Glu Asn Ile Lys Lys Gly Glu Gly Gln Pro Gly Ala  
225 230 235 240

Pro Gly Gly Lys Glu Asn Lys Leu Ser Val Leu Thr Val Pro Gln Ala  
245 250 255

Ile Leu Ala Ala Phe Val Ser Ala Phe Ala Pro Glu Gly Thr Lys Ile  
260 265 270

Glu Asn Lys Asp Leu Asp Pro Ser Thr Leu Tyr Pro Gly Gln Gly Ala  
275 280 285

Leu His Val Ile Glu Leu His Gln Asp Lys Ser Asp Trp Ser Ile Lys  
290 295 300

Val Leu Tyr Arg Asn Asn Asp Gln Met Lys Leu Lys Pro Met Lys Leu  
305 310 315 320

Ala Gln Cys Gly Asp Lys Cys Ser Tyr Gly Thr Phe Lys Ser Met Leu  
325 330 335

Gln Lys Tyr Asn Met Glu Lys Glu Ala His Asp Lys Leu Cys Lys Thr  
340 345 350

Ser

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGACGTTTTA CATAATTTAT CATGAGCTTC CTTCTCCATG TTATATTTTT GTAGCATTGA 60

TTTGAAAGTA CCATAAGAAC ACTTGTCAACC GCATTGTGCA AGTTTCATTG GTTTCAGCTT 120

CATTTGGTCA TTGTTTCTAT AGAGAACTTT TATGCTCCAA TCGCTCTTAT CTTGGTGTAG 180

TTCAATAACG TGAAGTGCTC CTTGGCCAGG ATATAAAGTA GACGGATCAA GGTCCTTATT 240

TTCAATTTTT GTACCTTCGG GAGCAAATGC TGAAACAAAT GCTGCTAAGA TAGCTTGAGG 300

AACGGTCAGC ACTGATAATT TGTTTCCTT TCCTCCTGGA GCACCCGGTT GTCCCTCTCC	360
TTTCTTTATG TTTTCGATAT CGTTCAATAT ATCGTTAAC ATACGACCTC CTGACATCTT	420
TCTAAGATTA TCATTAGAAG TCAAGGCGGT CCATAAATAT TTCTCAGAGA ATTGTTTAG	480
ATCTTGTTT ACAGTATTCC ACCATGTTGG AGCGTTATTT TGCTTGCTTT GTAAATTCAA	540
AGTTTCATAT GCCAGCCAAA CATTCTGAGG GCTTGTGTC GCATCTATTT TATACGCTTC	600
TTTTAATTTT GCAAGTGAAT TTTTATAATC TTTTGCACCT TTTGTTAAC A GTCTCTTAC	660
TGCTATTTC TGTTGTGCTA TGAAGTTGG ACAAGTTTT GGACTATAAA ATTTAGCATA	720
TTCACCAAAAC GAAGAAAATA TGGTTTATC TCCTTCTCT TTTGTCCAAA CTGCCTTTTC	780
CTTTTCTCT AGACCAGAAC CAATGATAAG CGCTCCTTCT TGAGATCTTC TCGTAGCACT	840
AGCTAATGTC CAATAATTT TATTTGAATC CCATTGTCA ACTTTAAAT TAGTTCTGTA	900
ATGTTCGGAT AATAATTGC CAATTTTAA TGCCCTTTCT TGACCTGCCG GTGTCAATTG	960
GCTTGAATCT TCAGACTTGT GTGTAATTT TGGACCGCCT GGATAATCAC AAGGTGTATG	1020
TGACATACCT CGTGCAGTCG CAAACACAAA TTTCAATTC	1059

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Xaa	Glu	Leu	Lys	Phe	Val	Phe	Val	Met	Val	Lys	Gly	Pro	Asp	His	Glu
1				5				10						15	
Ala	Cys	Asn	Tyr	Ala	Gly	Gly	Xaa	Gln							
				20				25							

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 406 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG GTT AAA GGT CCA GAT CAC GAA GCT TGT AAC TAT GCA GGA GGT CCT	48
Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro	
1 5 10 15	
CAG TTA ACT ACT CTT CAA GAA AAA GAT AGT GTT CTA ACT GAA GAT GGC	96
Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly	
20 25 30	
AAG ACA GAA GCA TAC GAA TTG GGA AAA CTT TTG GAC AAG GTA TAT AAA	144
Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys	
35 40 45	
AAA CAA TTA AAA GTT GAC AAA TGG GAT GCC ACG AAA ACC TAC TGG GCT	192
Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala	
50 55 60	
GTG TCC ACA AAA GCT ATG CGT ACT AAA GAA GCA GCC TTA ATT GTA GGA	240
Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly	
65 70 75 80	
GCA GGA TTG GAA AAT AAT CCT GCA AAA GCT AAA GGT AAT TGG ACA CAA	288
Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln	
85 90 95	
CAA CAG CTC GAT TCA ACA CAT TTT GAT GCG ATG CCT GGC TTT TCT AGA	336
Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg	
100 105 110	
TTT TGG AAT CCT CAA CAA TGT CCG GCA TAT TTC AGA GCG CTC TCG CTA	384
Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu	
115 120 125	
CAA AAT CAG AAA ATA AAG AAA T	406
Gln Asn Gln Lys Ile Lys Lys	
130 135	

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Val Lys Gly Pro Asp His Glu Ala Cys Asn Tyr Ala Gly Gly Pro

1

5

10

15

Gln Leu Thr Thr Leu Gln Glu Lys Asp Ser Val Leu Thr Glu Asp Gly  
                   20                 25                 30

Lys Thr Glu Ala Tyr Glu Leu Gly Lys Leu Leu Asp Lys Val Tyr Lys  
                   35                 40                 45

Lys Gln Leu Lys Val Asp Lys Trp Asp Ala Thr Lys Thr Tyr Trp Ala  
                   50                 55                 60

Val Ser Thr Lys Ala Met Arg Thr Lys Glu Ala Ala Leu Ile Val Gly  
                   65                 70                 75                 80

Ala Gly Leu Glu Asn Asn Pro Ala Lys Ala Lys Gly Asn Trp Thr Gln  
                   85                 90                 95

Gln Gln Leu Asp Ser Thr His Phe Asp Ala Met Pro Gly Phe Ser Arg  
                   100                 105                 110

Phe Trp Asn Pro Gln Gln Cys Pro Ala Tyr Phe Arg Ala Leu Ser Leu  
                   115                 120                 125

Gln Asn Gln Lys Ile Lys Lys  
                   130                 135

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AATTTCTTTA TTTTCTGATT TTGTAGCGAG AGCGCTCTGA AATATGCCGG ACATTGTTGA	60
GGATTCCAAA ATCTAGAAAA GCCAGGCATC GCATCAAAAT GTGTTGAATC GAGCTGTTGT	120
TGTGTCCAAT TACCTTAGC TTTTGCAGGA TTATTTCCA ATCCTGCTCC TACAATTAAG	180
GCTGCTTCTT TAGTACGCAT AGCTTTGTG GACACAGCCC AGTAGGTTT CGTGGCATCC	240
CATTTGTCAA CTTTTAATTG TTTTTATAT ACCTTGTCCA AAAGTTTCC CAATTCGTAT	300
GCTTCTGTCT TGCCATCTTC AGTTAGAACCA CTATCTTTT CTTGAAGAGT AGTTAACTGA	360
GGACCTCCTG CATAAGTTACA AGCTTCGTGA TCTGGACCTT TAACCAT	407

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAA GTT ATG GAT AAA TTG CGA AAA CAG GCA CCT CCT AAA ACT GAT GGC	48
Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly	
1 5 10 15	
AAT CCT CCA AAA ACA ACC ATA ATG AGT ACA CTT CAA AAG CAA CAA ATA	96
Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile	
20 25 30	
AGT TGC ACA GAA GTG AAA GCG GTT AAC TTA GAA AGT CAT GTT TGT GCT	144
Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala	
35 40 45	
TAT GAT TGT AGT CAA CCT GAA ACT GCA GGA ATT ACA TGC AAA GGA AAT	192
Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn	
50 55 60	
AAG TGT GAT TGT CCT AAA AAA CGC TAAAAATTAA TTCAAAACAT TTACATTTT	246
Lys Cys Asp Cys Pro Lys Lys Arg	
65 70	
TATTAATATT CAACTATCAA AAATTCTGTG TTGATTGTTA TTATATTTAT CATACTTACT	306
AGAAATAAAA TTTTATAACA TTGTTAATTC GAAATTGAAT ACACATAATA TTATAATTAG	366
TGAGGTTAAA AGAAATAAAC CGAATATCCA AATCAAAAAA AAAAAAAA AAAA	420

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Val Met Asp Lys Leu Arg Lys Gln Ala Pro Pro Lys Thr Asp Gly	
1 5 10 15	
Asn Pro Pro Lys Thr Thr Ile Met Ser Thr Leu Gln Lys Gln Gln Ile	
20 25 30	
Ser Cys Thr Glu Val Lys Ala Val Asn Leu Glu Ser His Val Cys Ala	
35 40 45	

Tyr Asp Cys Ser Gln Pro Glu Thr Ala Gly Ile Thr Cys Lys Gly Asn  
 50 55 60

Lys Cys Asp Cys Pro Lys Lys Arg  
 65 70

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTTTTTTTTT TTTTTTTTTT GATTTGGATA TTTCGGTTAT TTCTTTAAC CTCACTAATT	60
ATAATATTAT GTGTATTCAA TTTCGAATTA ACAATGTTAT AAAATTTAT TTCTAGTAAC	120
TATGATAAAAT ATAATAACAA TCAACACAGA ATTTTGATA GTTGAATATT AATAAAAAAT	180
GTAAATGTTT TGAATAAATT TTTAGCGTTT TTTAGGACAA TCACACTTAT TTCCCTTGCA	240
TGTAATTCCCT GCAGTTTCAG GTTGACTACA ATCATAAGCA CAAACATGAC TTTCTAAGTT	300
AACCGCTTTC ACTTCTGTGC AACTTATTTG TTGCTTTGA AGTGTACTCA TTATGGTTGT	360
TTTGGAGGA TTGCCATCAG TTTAGGAGG TGCCCTGTTT CGCAATTAT CCATAACTTC	420

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser	
1 5 10 15	
Thr Lys Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe	
20 25 30	
Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Cys Lys Ser Gln Cys	
35 40 45	
Gly Phe Gly Gly Ala Cys Gly Asn Gly Ser Thr Arg Pro Asn	
50 55 60	

Gln Lys His Cys Tyr Cys Glu  
 65                                   70

## (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Asp Lys Leu Gln Phe Val Phe Val Met Ala Arg Gly Pro Asp His  
 1                                   5                                   10                           15

Glu Ala Cys Asn Tyr Pro Gly Gly Pro  
 20                                   25

## (2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..26  
 (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGTGGATCCG TCAAAATGG TCACTG

26

## (2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1..28  
 (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCGGAATTCTG GTTATTCGCA ATAACAGT

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGCGGATCC GCATATGGAA GACATCTGGA AAGTTAATAA AAAATGTACA TCAG

54

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCGGAATTCT TATTTATTTT TTGGTCGACA ATAACAAAAG TTTCC

45

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAATTTGTAT TTTGTATATG GTATAAAGGA TCCATGATCA TGAAGC

46

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..37  
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGAACCAT GGATAATACA TCGATAAAGA TACTACG

37

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..17  
(D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTAAAACGAC GGCCAGT

17

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAAGTATATG GACTAAATTA GAGAGCAAGG C

31

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr Phe Asn Lys Leu Val Gln Ser Trp Thr Glu Pro Met Val Phe Lys  
1 5 10 15

Tyr Pro Tyr

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /label= primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

